



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 179985

TO: Sheridan Swope
Location: REM-2B71&3C60
Art Unit: 1656
Wednesday, February 22, 2006
Case Serial Number: 10/617443

From: Toby Port
Location: Biotech-Chem Library
REM-1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Examiner Swope,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Toby Port
X22523

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179986

From: Chan, Christina
Sent: Tuesday, February 21, 2006 12:56 PM
To: Swope, Sheridan; STIC-Biotech/ChemLib
Subject: RE: 10/617,443

~~Please rush. Thanks~~ Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

CRFL

-----Original Message-----

From: Swope, Sheridan
Sent: Tuesday, February 21, 2006 12:11 PM
To: Chan, Christina
Subject: 10/617,443

Chris, May I have this rushed for an AF allowance?

For 10/617,443, pls interference search only:

SID 1 against the NT and AA databases.

SID 2 against the NT and AA databases.

Thanks,

Sheridan Swope, Ph.D.
Patent Examiner, AU 1656
Recombinant Enzymes
571-272-0943 (voice)
E02B71 Remsen Bld (Office)
E03C70 Remsen Bld (Mailbox)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 18:07:50 ; Search time 512 Seconds
(without alignments) 10436.231 Million cell updates/sec

Title: US-10-617-443b-1

Perfect score: 3006

Sequence: 1 caggagactcgaagttgcag.....gcccaaaaaaaaaaaaaa 3006

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/prodata/1/ina/1_COMB_seq:*
- 2: /cgn2_6/prodata/1/ina/5_COMB_seq:*
- 3: /cgn2_6/prodata/1/ina/6A_COMB_seq:*
- 4: /cgn2_6/prodata/1/ina/6B_COMB_seq:*
- 5: /cgn2_6/prodata/1/ina/6_COMB_seq:*
- 6: /cgn2_6/prodata/1/ina/PCTUS_COMB_seq:*
- 7: /cgn2_6/prodata/1/ina/PP_COMB_seq:*
- 8: /cgn2_6/prodata/1/ina/RE_COMB_seq:*
- 9: /cgn2_6/prodata/1/ina/backfilest1_seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	385	12.8	1894	US-10-104-047-795	Sequence 795, App
2	385	12.8	2036	US-09-949-016-399	Sequence 399, App
3	384.6	12.8	2036	US-08-923-454A-17	Sequence 17, App1
4	383.4	12.8	2205	US-08-888-077A-41	Sequence 41, App1
5	383	12.7	1521	US-09-949-016-4643	Sequence 4643, Ap
6	322.8	10.7	1859	US-09-724-864-22	Sequence 22, App1
7	290.6	9.7	1835	US-08-923-454A-7	Sequence 7, App1
8	290.6	9.7	2040	US-09-075-460-4	Sequence 4, App1
9	290.6	9.7	2187	US-08-923-454A-23	Sequence 23, App1
10	290.6	9.7	2187	US-08-923-454A-24	Sequence 24, App1
11	290.6	9.7	2476	US-09-008-271A-23	Sequence 23, App1
12	290.6	9.7	2476	US-09-968-415-23	Sequence 23, App1
13	289	9.6	2187	US-08-923-454A-30	Sequence 30, App1
14	227	7.6	539	US-08-322-742-18	Sequence 18, App1
15	217.8	7.2	1503	US-08-923-454A-5	Sequence 5, App1
16	217.8	7.2	1787	US-08-923-454A-28	Sequence 28, App1
17	208	6.9	2551	US-08-923-454A-3	Sequence 3, App1
18	208	6.9	2551	US-08-923-454A-26	Sequence 26, App1
19	128.2	4.3	57299	US-09-949-016-1241	Sequence 1241, A
20	128.2	4.3	57299	US-09-949-016-1241	Sequence 1241, A
21	125.4	4.2	732	US-08-923-454A-1	Sequence 1, App1
22	121.8	4.1	1332	US-09-902-540-4672	Sequence 4672, Ap
23	121.8	4.1	24754	US-09-902-540-1230	Sequence 1230, Ap
24	112.8	3.8	1260	US-09-902-540-8673	Sequence 8673, Ap

c	25	112.8	3.8	9191	3	US-09-902-540-918	Sequence 918, App
	26	112.6	3.7	1771	3	US-08-818-112-13	Sequence 13, App1
	27	112.6	3.7	1771	3	US-08-818-111-13	Sequence 13, App1
	28	112.6	3.7	1771	3	US-09-056-556-13	Sequence 13, App1
	29	112.6	3.7	1771	3	US-09-072-596-13	Sequence 13, App1
	30	112.6	3.7	1771	3	US-09-072-596-13	Sequence 13, App1
	31	112.6	3.7	1771	3	US-10-193-002-13	Sequence 13, App1
	32	112.6	3.7	1771	3	US-10-084-843-13	Sequence 13, App1
	33	112.6	3.7	4403765	3	US-09-103-840A-2	Sequence 2, App1
	34	112.6	3.7	4411529	3	US-09-103-840A-1	Sequence 1, App1
	35	109.6	3.6	1395	3	US-09-712-363-36	Sequence 36, App1
	36	106.8	3.6	1224	3	US-09-252-991A-9171	Sequence 8171, Ap
c	37	106.8	3.6	1380	3	US-09-252-991A-7981	Sequence 7981, Ap
	38	102.6	3.4	1650	3	US-09-712-363-44	Sequence 44, App1
c	39	102	3.4	1167	3	US-09-902-540-5297	Sequence 5297, Ap
	40	102	3.4	30783	3	US-09-902-540-1258	Sequence 1258, Ap
	41	101	3.4	38675	3	US-08-311-731A-135	Sequence 135, App
c	42	100.2	3.3	1488	3	US-09-489-039A-5255	Sequence 5255, Ap
	43	100.2	3.3	1494	3	US-09-489-039A-5193	Sequence 5193, Ap
	44	100	3.3	495	3	US-09-702-705-897	Sequence 897, App
	45	100	3.3	495	3	US-09-736-457-897	Sequence 897, App

ALIGNMENTS

RESULT 1									
US-10-104-047-795									
; Sequence 795, Application US/10104047									
; Patent No. 6943241									
; GENERAL INFORMATION:									
; APPLICANT: HELIX RESEARCH INSTITUTE									
; TITLE OF INVENTION: NO. 6943241el full length cDNA									
; FILE REFERENCE: H1-A0105									
; CURRENT APPLICATION NUMBER: US/10/104.047									
; PRIOR FILING DATE: 2002-03-25									
; PRIOR APPLICATION NUMBER:									
; PRIOR FILING DATE:									
; NUMBER OF SEQ ID NOS: 4096									
; SOFTWARE: PatentIn Ver. 2.1									
; SEQ ID NO 795									
; LENGTH: 1894									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-10-104-047-795									
Query Match									
Best Local Similarity 63.8%; Pred. No. 6.7e-83;									
Matches 630; Conservative									
Mismatches 330; Indels 27; Gaps 2;									
QY	1027	CGCCAGCGCAGGTCCTCCACGCTGAGCAGCCCGCTCAAGTTCAAGTTCACTTCTG	1086						
DB	364	CCTGCGGCGCAGGCGAGGAGATCCCAAGTTGCGCATTAATTAATTATCTTATCGCG	423						
QY	1087	ACGTGTGGAAGAATCGCACAGCGCGTGTCCATCATGAGTCTTCTGTGAGACACCGC	1146						
DB	424	ACGTGTGGAAGAATCGCCCTCTGCGTGTTCATCATGATTTTGTGCAAGCTTCCGT	483						
QY	1147	TGTTGGCGCGCAACGTGCGCTTGCACGCTTGTGCTTCATCATGTGTGAGCGCGC	1206						
DB	484	TTTCTAAACGAGAGGTGCGGTCGTAGTGGTCTGTGTTATTTGTGTGGAATGAGC	543						
QY	1207	TGATCATCAACCATGCCCGCTGTGTGTTCAGCAAGTGTGCCCCGGGCGAGCAGC	1266						
DB	544	TGATGTGTAACAATCCACGCTGTGACCAACAA-----GCACCGGG	585						
QY	1267	TCAAGTGAGTACAGATGGGAGCTCTTATGAGCCACCATCAAGATCGACAAGA	1326						
DB	586	TCAAGTGAGTACAGATGGGAGCTCTTATGAGCCACCATCAAGATCGACAAGA	645						
QY	1327	AGTCGACATTCGACATCAAGATCATCCCAAGAAAAGCTCTGTGTGTGTGCTGG	1386						
DB	646	AAGCAGATCGCATCTCATTAATAATTGACCAACGAGGCAAGGCTGCTGCTGCTGG	705						

QY	1387	GTCAATCGGCGAAGCTGGGGGCTGGGGAGTTTGTGGTGGCCATCGGGAGTCCCTTCGGCC	1446
Db	706	GCCCTCTCTCAAGCTGGGGCCGGAGAGTTGTGTGTGCGCATCGAAGCCCGTTTCTCC	765
QY	1447	TACAGAACACAGTGCACACGGGCATCGTCAGCACTGCCAGCGGGAGGGCAGGAGCTGG	1506
Db	766	TTCAAAAACACAGTCCACACCGGGATCGTGAAGCACCAACGAGGAGGGCAAGAGCTGG	825
QY	1507	GCCCTCGGGGACTCCGACATGTGACTATCCAGACGGATGCCATCATCACTTACGGGAACT	1566
Db	826	GGCTCCGAACTCAACATGAGCTTACATCCAGACCGAGCCATCATCACTATGTGAAACT	885
QY	1567	CCGGGGGACCACTGGTGAAGCTGTGATGGCGAGAGTCAATTGGGCATCAACACGCTCAAGGTCA	1626
Db	886	CGGAGAGCCCTGTAGTAACTCGACGGTGAAGTATTTGAAATTACACTTTGAAATGA	945
QY	1627	CGGCTGGCATCTCTTTGGCCATCCCTTCAGACCGCATCACAGGTCTCTCAAGATTC	1686
Db	946	CAGCTGGAAATCTCTTTCAATCCCATCTGATTAAGATTAAAGTTCTCTCAAGAGTCC	1005
QY	1687	AAGACAGCAATCAAG-----ACTGGAAGAGCGGTTGATGGCATAGGATGC	1737
Db	1006	ATGACCGACAGGCCCAAGAGAAAAGCCATCACAGAGAAAGTATTTGTGATCCGAATGA	1065
QY	1738	GGAGGATCACACCAAGCCTGGTGTGATGAGTGAAGGCCAGCAACCGGACTTCCAGAGG	1797
Db	1066	TGTCACTCAGCTCGAGCAAGGCAAGAGAGTGAAGAGACCGGACACCGGACTTCCAGAGG	1125
QY	1798	TCAGCAGTGGAAATTTATGTGCAAGAGGTGGCGCCGAATTCACTTTTCAGAGAGCGCGCA	1857
Db	1126	TGATCTCAGGACGGTATTTAAATTGAAGTAATTCCTGAATACCCAGCAGAACTGTGTGTC	1185
QY	1858	TCCAAGATGTGACATCATCGTCAAGGTCAACGGGCGTCTCTAATGGGACTCGAGTAGC	1917
Db	1186	TCAAGAAAACGACGTCTATATTCAGCATCAATGACAGTCCGTGCTCTCCGCCATATGATG	1245
QY	1918	TGACAGAGCCGTGTCTGACCGAGTCTCTCTCTAATGAGAGTGCAGGCGGGAGACGAGC	1977
Db	1246	TCAGCGACGTATTTAAAGGAGAAAGCACTGAAACATGTGTGTCTCGAGGGGTATATAGG	1305
QY	1978	ACCTCTCTTTAGCATCGCACTTAGG	2004
Db	1306	ATATCATGATCACAGTGAATTCGAGG	1332

RESULT 2
 US-09-949-016-399
 Sequence 399, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: C1001107
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 399
 LENGTH: 2036
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-399

Query Match	12.8%;	Score 385;	DB 3;	Length 2036;
Best Local Similarity	63.8%;	Pred. No. 6.9e-83;		

Matches 630; Conservative 0; Mismatches 330; Indels 27; Gaps 2;

QY	1027	CCGACGACGAGGTCTCCACGACGTCGACACCGCCGCTCAAGTTCACATTCATGCTG	108
Db	509	CCTGCGGCGCAAGGCGAGAGATGCCAACATGTTTGGCGCATTAATATTAATTCGCGG	568
QY	1087	ACGTGATGAGAAAGATCGCACGACCGTGGTTCACATGAGCTCTTCTGAGACACCCG	1144
Db	569	ACGTGATGAGAAAGATCGCCCTCGCGGTTCATATGAAATGTTTGGCAAGCTTCCGT	628
QY	1147	TGTTTGGCGCAACGTGCCCTGTCTCAGCGGTTCTGCGCTTATCATGTCTCAGAGCCGCG	1206
Db	629	TTTCTAAACGAGAGGTGCGGTTGCTATGAGGTCTGGTTTATGTGTTCGAAAGATGAC	688
QY	1207	TGATCATCAACCATGCCCCAGTGGTGTCCAGCAACAGTGTGCCCCGGGACGACAGC	1266
Db	689	TGATGTGTACAAATGCCCCACGTTGGTGAACAA-----GCACCCCG	730
QY	1267	TCAAGGTGACGTCACAGAAATGGGGATCTCTTATGAGGCCACCATCAAGACATCGACAG	1322
Db	731	TCAAGTTGAGACTGAAGAACGTGTCACATTACGAAGCCAAATCAAGATGTGATGAG	790
QY	1327	AGTGGACATTTGCCACCATCAAGATCCATCCCAAGAAAAAGCTCTCTGTGTGTTCTGG	1386
Db	791	AAGCAGACATGCACTCATCAAAATGACACACAGGGGCAACGTCTGTCTGTGCTTGG	850
QY	1387	GTCACTGGGCGGACCTGGGCGCTGGGGAGTTTGTGATGGCCATGGGACGTCCTTCCGCT	1446
Db	851	GCCGCTCTCAGAGAGTGGGCGGGAGAGTTCTGTGTGCGCATCGGAAGCCCGTTTCCC	910
QY	1447	TACAGAACACAGTGAACAAGGGCATTCGTACGACCTGCCACGCGGAGGGACGGAGCTGG	1506
Db	911	TTCAAAACACAGTACACACCGGGATCTGTGACACACACCACGAGGCGGCAAAAGCTGG	970
QY	1507	GCTCCCGGGAATCCGGAACATGGAATCAATCCAGACGGAATGCCATATCAACTACGGGAAT	1566
Db	971	GGCTCCGACATTCAGACATGGAATCAATCCAGACCGAGCCGATCATCACTATGAAACT	1030
QY	1567	CCGGGGGACCACTGGTGAACCTGGATGGCGAGGTCAATTGGCATCAACGCTCAAGTCA	1626
Db	1031	CGGAGAGGCGCTTGTATTAACCTGGACGGTGAAGTGAATTGGAATTAACTTTGAAAGTGA	1090
QY	1627	CGGCTGGGATCTCTTTGGCATTCGCCCTCAGACCGCATCAACGGTCTCTCAACAAGTCC	1686
Db	1091	CAGCTGGATCTCTTTGGCAATCCCATCTGTATTAAGATTAAAAAGTTCTCTCAGAGTCCC	1150
QY	1687	AAGAACAAGCATCAAG-----ACTGGAAGAAAGCGCTTATCGGCAATACGATGC	1737
Db	1151	ATGACCGACAGGCCAAAGAAAAAGCCATCAACAAAGAAAGATATATGTTTCGAATGA	1210
QY	1738	GGAAGATTCACACAAAGCTGTGATGAGCTGAAGGCCAGAACCCGGAATTTCCACAGG	1797
Db	1211	TGTACATCAAGTCCAGCAAAAGCTGAAGAGAACCGGACCGGAGCTTCCACAGCG	1270
QY	1798	TCAGCAGTGAATTTATGTGCAAGAGGTGGCGCGAATTCACTTCTCAGAGAGCGGCA	1857
Db	1271	TGATCTCAGAGGCGTATATTAATTAAGTAATTTCTGATTAACCCAGCAAGAACTGTGCTC	1330
QY	1858	TCCAAGATGTGAATCATCTGTCAAGGTCAACGGGCGTCTCTGTGTGGAATCTGAGTAGC	1917
Db	1331	TCAAGGAAACGAGGTCAATATCGATCAATGAGACAGTCCGTGTCTCTCGCCATATGTG	1390
QY	1918	TGCAAGAGGCGGTCTGACCGAGTCTCTCTCTACTAGAGAGTGGCGGCGGGAACGACG	1977
Db	1391	TCAGCGAGCTATTAAGAAAGGAAAGCAACCTGAACATGTGTGTCTCGCAGGGTATATGAG	1450
QY	1978	ACCTCTCTTTCAGCATCGACCTGAGG 2004	
Db	1451	ATATCATGATCAAGTATTTCCCAAG 1477	

RESULT 3
US-08-923-454A-17

Sequence 17, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasey, Caretha
APPLICANT: Liyi, George
APPLICANT: Karian, Eric
APPLICANT: Clinkbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE: Feature polymorphism at 1325
US-08-923-454A-17

Query Match 12.8%; Score 384.6; DB 3; Length 2036;
Best Local Similarity 63.7%; Pred. No. 8,6e-83;
Matches 629; Conservative 1; Mismatches 330; Indels 27; Gaps 2;

QY 1027 CCGCAGGCGAGGTCTCCACCAAGTGGAGAGCCCGGCTACCAAGTTCAAGTTCAATCTGCTG 1086
DB 509 CCGGCGGCGCAGGAGGAGGAGATCCCAAGTTGGCGCATTAATACTTATCGCGG 568
QY 1087 AGCTGTGAGAGAAATCCGACAGCGGTGTGCAACATAGAGTCTTCCCTGAGACACCGCG 1146
DB 569 AGGTGTGAGAGAGATCGCCCTGCGGTGTTCATATCAAAATGTTTGGCAAGCTTCCGT 628
QY 1147 TGTTCGCGCAGAGCGTCCCTGTCCAGCGGTTTGGCTTCAATGTCAAGAGCGCGGC 1206
DB 629 TTTCTTAAGAGAGAGTGGCGGTGTGCTAGTGGGTCTGGTTATGTGTGCGAAGATGAGC 688
QY 1207 TGAATATCAACCAATGCCAGAGTGTGTCCAGCAACAGTGTCTGCGCGGCGAGCGAGC 1266
DB 689 TGATCGTGAACAATGCCAGAGTGTGTGACCAACAA-----GCACCGGG 730
QY 1267 TCAAGGTGAGCTACAGATGGGAGCTCTATGAGGCCACCATCAAGAATCGACAAAGA 1326

DB 731 TCAAGGTGAGCTGAGAGAGCGTGTGCACTTACGAAAGCAAAATCAAGATGTGATGAGA 790
QY 1327 AGTGGACATTTCCACCAATCAAGATTCATCCCAAGAAAAGCTCCCTGTGTGTTGCTGG 1386
DB 791 AAGCAGACATCGCATCTCAAAATTGACCAACAGGGCAAGCTGCTCTCCGTGCTTGG 850
QY 1387 GTCACTCGGCGGACCTGTGGGCTGGGAGTTTGTGTGTGCGCATGGGAGTCCCTCGGCC 1446
DB 851 GCGGCTCTCTGAGGTGCGGCGGAGAGTTGTGTGTGCGCATGCGAAGCCGTTTCC 910
QY 1447 TACAGAACAGTGAACAAGGAGCATTCGTACAGACTGCCAGCGGAGGAGGAGAGCTGG 1506
DB 911 TTCAAAACAGTACCAACCGGAGTGTGAGACCAACCAAGAGGCGGCAAAAGCTGG 970
QY 1507 GCTTCGGGACTCCGACATGACATTCATCCAGAGCGGATCCATATCAATACGGAAC 1566
DB 971 GGTCCGCACTGACAGATGACATTCATCCAGAGCGGATCCATATCAATATGAAACT 1030
QY 1567 CCGGGGACCACTGTGTAACTGTGATGGCGAGTCAATTGGCATCAACGCTCAAGTCA 1626
DB 1031 CGGAGGCGCTTGTGTAACTGTGACGAGTGAATGATTAACCTTTGAAGTGA 1090
QY 1627 CGGCTGCGATCTCTTGTGCAATCCCTGACAGCGGATCAACGCTTCTCAAGAGTCC 1686
DB 1091 CAGCTGAAATCTCTTGTGCAATCCATCTGATTAAGATTAAGATTAAGATTAAGATTA 1150
QY 1687 AAGACAGCAGATCAAG-----ACTGAGAGAGCGCTTCAATCGGCATACGAGTGC 1737
DB 1151 ATGACCGCAGGCGCAAGAAAGCAATCAACCAAGAAAGATATTTGTGTATCCCAATGA 1210
QY 1738 GAGCATCAACCAAGCCTGTGTGATGAGCTGAAGGCGAGCAACCGGACTTCCAGAGG 1797
DB 1211 TGTCACTACGTCGCAAGAGCAGGAGTGAAGAGCGGACCGGAGCTTCCAGAG 1270
QY 1798 TCAGAGTGAATTTATGTGCAAGAGGTTGGCGCGCAATTCACCTTCTGAGAGGCGGCA 1857
DB 1271 TGATTCAGAGACGATTAATTAATGAGATTAATTCGATACCCAGCAGAGCTGTGTC 1330
QY 1858 TCAGAGTGTGACATCATCTGTAAGGTCACAGCGGCTCTTGTAGTGAATCGAGTACG 1917
DB 1331 TCAAGAAAGAGAGCTCATTAATCAAGCATCAATGACAGTCCGTGTCTCCGCAATGATG 1390
QY 1918 TGCAGAGAGCGGTGTGACCGAGTCTCTCTCTTCTGAGAGTGTGGGCGGAGAGCAG 1977
DB 1391 TCAAGGAGCTCATTAAGAGGAGAAAGACCTGAAACATGTGTGTCCGAGGGTAAATGAG 1450
QY 1978 ACCTCCTTTCAGATCGACCTGAG 2004
DB 1451 ATATCATATCACTGATGATTCGCGAAG 1477

RESULT 4
US-08-888-077A-41
Sequence 41, Application US/08888077A
Patent No. 6020143
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE AND USES THEREFOR.
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: LERNER, DAVID, LITENBERG, KRUMHOLZ & MENTLIK
STREET: 600 SOUTH AVENUE WEST
CITY: WESTFIELD
STATE: NJ
COUNTRY: USA
ZIP: 07090-1497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/888,077A
/ FILING DATE: 03-JUL-1997
/ CLASSIFICATION: 530
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: US 08/592,541
/ FILING DATE: 26-JAN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PALISI, THOMAS M
/ REGISTRATION NUMBER: 36,629
/ REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 654-5000
/ TELEFAX: (908) 654-7866
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2205 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 1..2205
/ OTHER INFORMATION: /note="multTm1-TM2"
US-08-888-077A-41

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Query Match      12.8%; Score 383.4; DB 3; Length 2205;
Best Local Similarity 63.7%; Pred. No. 1.7e-82;
Matches 629; Conservative 0; Mismatches 331; Indels 27; Gaps 2;

Qy 1027 CCGCCAGCGCAGCTCTCCACAGCTGAGCAGCCCGCGCTCAAGTTCACTTCATGCTG 1086
Db 585 CCTCCGCGCAGAGGCGCAGGAAGATCCCAAGTTGCGCCATTAATACCTTATGCGCG 644

Qy 1087 ACGTGTGAGAGATGCGACACCGCTGCTCCATAGAGCTCTTCTGAGACCCGCG 1146
Db 645 ACGTGTGAGAGATGCGACCCCTCCCGCTGCTCATATGGAATTTTTCGCAAGCTTCGT 704

Qy 1147 TGTTCGCGCGCAAGTGCCTCTGTCAGCGGCTTCTGCTTCATATGTCAGAGCGCGCC 1206
Db 705 TTTCTAAACGAGAGGTGCGGCTGCTGCTAGTGGGTCTGGGTTTATGTGCGGAATGAGAC 764

Qy 1207 TGATCATCAACATGCGCAGGTGTGTCAGCAACAGTCTGCGCCCGGCGAGCAGCAGC 1266
Db 765 TGATGTGACAAATGCCACGCTGTGACCAACAA-----GCACCGCG 806

Qy 1267 TCAAGTGTGAGTACAGAAATGGGGGCTCCTATGAGGCGCAGCATCAAGACATCGACAGA 1326
Db 807 TCMAAGTTGAGCTGAAGAACGCTGCGCTTACGAAAGCCAAATCAAGATGTGATGAGA 866

Qy 1327 AGTCGAGATTCGCCACATCAAGATCATCCCAAGAAAAAGCTCCCTGTGTTGCTGCG 1386
Db 867 AAGCAGACATGCGCATCATCAAAATTTGACACACAGGCGCAAGTGTCTGCTGCTG 926

Qy 1387 GTCACTCGGCGCACTCTGCGGCGCTGCGGAGTTGTGTGCGCCATCGGAGTCCCTCGCC 1446
Db 927 GCGGCTCTCTCAAGCTGCGGCGCGGAGAGTTGTGTGCGCCATCGGAAAGCCGTTTCC 986

Qy 1447 TCAGAGACAGAGTGAACGCGCATGTCAGCATGTCGCCAGCGGAGGAGGAGGAGCTGG 1506
Db 987 TTCMAAACACAGTCAACACCGGATGTGTAGCACCCAGCGAGGCGGCAAAAGAGTGG 1046

Qy 1507 GCGTCCGGAATTCGACATGAGTACATCAAGACGAGTCCCATCAATCACTAGGGAATCT 1566
Db 1047 GCGTCCGGAATTCGACATGAGTACATCAAGACGAGTCCCATCAATCACTAGGGAATCT 1106

Qy 1567 CCGGAGGAGCACTGAGGAGCTGAGTGGCGAGGCTCAATTGCAACAAGCTCA 1626
Db 1107 CCGGAGGAGCCGTTAGTAACTGAGAGGAGTGAATTTAACTTTGAAAGTGA 1166

Qy 1627 CGGCTGGCATCTCTTGGCCATCCCTCAAGCCGATCAAGGTTCTCTCAAGAGTTCC 1686

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Db 1167 CAGCTGGAATCTCTTTCAGATCCCATCTGATTAAGTTAAAGATTCTTCAGGAGTCCC 1226
Qy 1687 AAGCAGACAGATCAAAAG-----ACTGGAAGAGCGCTTCATCGGCAATACGATGC 1737
Db 1227 ATGACCGACAGGCGCAAGGAAAGAACCATCCACCAAGAAAAAGTATATGATTCGAAATGA 1286
Qy 1738 GAGACATCAACCAAGCTGTGATGAGCTGAAGGCGCAGCAACCGGACTTCCAGAG 1797
Db 1287 TGTCACTCAGCTCCAGCAAAAGCCAAAGAGCTTGAAGACCGGCAACCGGACTTCCAGAG 1346
Qy 1798 TCAGCAGTGAATTTATGTCCAAAGAGTTGCGCCGAATTCACCTTCTCAGAGAGCGGCA 1857
Db 1347 TGATCTCAGAGAGCGTATATATTAATGAAGTATTCCTGATACCCAGCAGAAAGTGTGTC 1406
Qy 1858 TCAGAGATGTGATCATCATGTCAGAGTCAAGCGGCGCTCTAGTGAATTCAGAGTGAAGC 1917
Db 1407 TCAAGGAAACGAGGTATATATGACATCAATGAGCAGTCCGTGCTCCGCAATGATG 1466
Qy 1918 TCAGAGAGGCGGCTGACCGAGTCTCTCTCTACTGAGAGTGCAGGCGGAGAGAGCAGC 1977
Db 1467 TCAGGACGTATATTAAGGAAAGAACCCCTGAACATGATGTGTCGAGGAGTAAAG 1526
Qy 1978 ACTCTCTTCAGAGATCGCAGCTGAGC 2004
Db 1527 ATATCATGATCAAGTGAATTCGCAAG 1553

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RESULT 5
US-09-949-016-4643
/ Sequence 4643; Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4643
/ LENGTH: 1521
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-4643

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Query Match      12.7%; Score 383; DB 3; Length 1521;
Best Local Similarity 64.0%; Pred. No. 1.9e-82;
Matches 625; Conservative 0; Mismatches 325; Indels 27; Gaps 2;

Qy 1037 AGCTCTCACACAGTGAAGAGCCCGGCTCAAAAGTTCAATTCATGTCGAGTGTGA 1096
Db 1 AGGCGAGAGAGATCCCAAGTTGGCGCAATTAATTAATCTTATGCGGAGCTGTGTGA 60

Qy 1097 GAAGATGCGACAGCGGTGTCCACATAGAGCTCTTCTGAGACACCGCTGTGGCGG 1156
Db 61 GAAGATGCGCCCTGCGCTGTCTATATGAAATGTTTCGAAAGCTTCCGTTTCTAAAG 120

Qy 1157 CAAGTCCCTCTGTCAGCGGTTCTGCTTCATCATGTCAGAGCCGCGCTGATCATAC 1216
Db 121 AGAGTCCCGGTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 180

Qy 1217 CAATGCCAGCTGTGTGTCAGCAACAAGTGTGCTGCCCGGAGCAGCAGCTCAAGTGA 1276
Db 181 AATGCGCAGGTGTGACCAACAA-----GCACCGGCTCAAAAGTTGA 222

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Qy	127	GCTACAGAAATGGGGACCTCTTATGAGGCGACCATCAAAACATTCAGCAAGAAAGTGGACAT	1336
Db	223	GCTGAGAGACGTGCTGCATTACGAGGCCAAATTCAGATGTGGATGAGAAACAGACAT	282
Qy	1337	TGCCACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTGTGTGTGTGCTGGGTCACTCGGC	1398
Db	283	CGCACTATCAAAATTAATGACACACAGGGGCAAGTGTCTGTCTCTGCTGTGGCGCTCTC	342
Qy	1397	CGACCTGCGGCTTGGGAGTTTGTGTGTGGCCATTCGGCAGTCCCTTGCCTTACAGAACAC	1458
Db	343	AGAGCTGCGGCGGGGAGAGTTGTGTGTGCGCATCGGAAGCCGTATTTCTTCAAAACAC	402
Qy	1457	AGTACAAACGGGCAATCGTCACACCTGCCACGCGGAGGGGACGGGACGTGGGCTCCCGGA	1516
Db	403	AGTACCAACCGGAGATCGTAGACACACCCAGGAGGCGGCAAAAGGCTGGGGCTCCGGA	462
Qy	1517	CTCCGACATGGACTTACATCCAGACGGATGCATCATCACTACGGGAATCCCGGGGAC	1576
Db	463	CTCAGACATGGACTTACATCCAGACGGCATATCACTTGAAGAACTGGGAGGCC	522
Qy	1577	ACTGCTGAACCTGATGGCGAGGTCAATTGGCATCAACGCTCAAGCTCACGGCTGGCAT	1638
Db	523	GTTAGTAAACCTGACCGGTGAAGTGAATTGAATTAACATTGAAGTGAAGCTGGAT	582
Qy	1637	CTCCTTTGCCATCCCTCATAGACCGCATCAACGGTTCTTCAAGATTCCAGACAGCA	1698
Db	583	CTCCTTTGCCATCCCATCTGATGAATTAAGTTTCTTCAACGGAGTCCCATGAACGACA	642
Qy	1697	GATCAAG-----ACTGGAAGAGACGGCTTCACTGGCATACGGATGCGGACGATCAC	1747
Db	643	GCGCAAGGAAAAGCCATCACAGAGAAAGTATTTGTATCCGAATGATCTAC	702
Qy	1748	ACCAAGCTGTGTGATGAGCTGAAGGCGAGCAACCCGACCTTCCAGAGGTCAAGCTGG	1807
Db	703	GTCAGACAAACCAAGACGTGAAGAGACCGGACCGGACCTTCCAGACGTGATTCAGG	762
Qy	1808	AATTTATGTGCAAGAGTTTGCGCGGCAATTCACTTCTCAAGAGGCGGCATTCAGATGG	1867
Db	763	AGCGATATTAATTGAAGTATTTCTTGATACCCACAGCAAGCTGTGTCTCAAGSAAA	822
Qy	1868	TGACATCATCGTCAAGGTCAACGGGCGTCTCTGTGTGACCTCGATGAGCTGACGAGAGC	1927
Db	823	CGACGTCAATTAATCAGCATTAATGACAGTCCGTGTCTCCGCAATGATGTACGACGT	882
Qy	1928	CGTGTGACCGAGTCTCTCTCTCTTACTGAGAGGTGCGGCGGGAACGACACTTCTT	1987
Db	883	CATTAAAGGGAAGACACCTCTGAACATGTGTGTCGACGGGTAAATGAATATCATAT	942
Qy	1988	CAGCATGCGACCTGAGG 2004	
Db	943	CACAGTATTCGCCGAG 959	
RESULT 6			
US-09-724-864-22			
Sequence 22, Application US/09724864			
Patent No. 6380362			
GENERAL INFORMATION:			
APPLICANT: Watson, James D			
APPLICANT: Multison, James G.			
TITLE OF INVENTION: Polynucleotides, polypeptides expressed			
FILE REFERENCE: 11000.1050U1			
CURRENT APPLICATION NUMBER: US/09/724,864			
PRIOR APPLICATION DATE: 2000-11-28			
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678			
PRIOR FILING DATE: 1999-12-23			
NUMBER OF SEQ ID NOS: 72			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 22			
LENGTH: 1859			
TYPE: DNA			
ORGANISM: Mouse			

Query Match	10.7%	Score 322.8	DB 3	Length 1859
Best Local Similarity	63.3%	Pred. No. 6.9e-66		
Matches 542	Conservative 0	Mismatches 287	Indels 27	Gaps 2
QY	1170	TTCCAGCGGTTCTGGCTTCATCATGTCAGAGGCGCGGCTGATCATCACCATTAGGCCACGTG	1229	
DB	367	TTCCAGCGGCTCTGGGTTTCAAGTCTGAGGAGTGGCTCATTTGTACCAATGCCACGTC	426	
QY	1230	GTGTCACGCAACAGTGTGCGCCCGGCGAGGCGAGCTCAAGGTGAGCTACAGATTGG	1289	
DB	427	CTACACCAACCA-----GCGAAGATCCAGGTAGAGCTCCAGGCGG	468	
QY	1290	GACTCTTATGAGGCGCACATCAAGACATGACAGAAAGTCGACATTGCCACATCAAG	1349	
DB	469	GCCCGGTATGAGGCCACCGTCAAGACATGACCATTAACCTGGACCTTGGACCTGATTAA	528	
QY	1350	ATCATATCCAAAGAAAGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1409	
DB	529	ATTCAGGCGAGTTACTGAGCTTCAGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	588	
QY	1410	GGGAGTTTGT	1469	
DB	589	GGAAGTTTGT	648	
QY	1470	ATCTGTACGACCTGCGCAGCGGAGGGGAGGAGGAGCTGGGCTTCGCGGACTCCGACAT	1529	
DB	649	ATTGTGTACGACCAACAGAGAGGGGGGAGAGAGCTGGGACTGAAGAAATTGACATTA	708	
QY	1530	TACATCCAGACGATGCTCATCATTAACGAGAACTTCGGGGGACCACTGTGTGACCTG	1589	
DB	709	TATATCCAGACGATGCTCATCATTAACGAGAAATTCTGGGGGCTCGCTGTGTGACCTG	768	
QY	1590	GATGCGGAGGCTCATTTGSCATCAACAGCTCAAGGCTGACGCTGGCATCTCTTTGCCATC	1649	
DB	769	GATGCGGACGATGATGATTAACACTCTGAGGTGACTGAGGAGATCTCTTTTGGCATC	828	
QY	1650	CCCTCAGACCGCATCACACGGTTCCTTCACAGATTCCAGACAGATCAAGCATCAAGAC--	1706	
DB	829	CCCTCTGATGGGATCAACAGATCTCTGGAAGACTATCATGAGCGCGATTGAAGGCAAG	888	
QY	1707	-----TGAAAGAGCGCTTCATGCGCATACGATGCGGACGATCAACCAAGCTGTGTG	1760	
DB	889	GCCTCTTGGAGAAAGATTAACCTGGGCTCTTCGATGCTGCTCTCACTGTGAACCTCTT	948	
QY	1761	GATGAGCTGAAGCGCACACACCGGACTTCCCGAGGCTCAGAGTGAATTTATGTCGA	1820	
DB	949	CAGGAAATGGAAGAGGCAAGATCCAGATCTCTGTATGTGATGTGAGTTTGTATAT	1008	
QY	1821	GAGGTTCCGCGGAATTCACCTTTCAGAGAGGCGGCATCCAGATGTGTGACATCATGCT	1880	
DB	1009	GAAATGATTAAGGATGTGGCTGTCTGCAAGCTCGGGGTTGAGAGACATGATGTAATGTCT	1068	
QY	1881	AAGGTCAACGGGCGCTTCCTTATGTGACTCGAGTGAAGCTGAGAGAGCGGTGTGACCGAG	1940	
DB	1069	AGCATTAACGGGCAACCTGTACCAACCAACATGATGTCTATTGAAGCTGTTAAGCAAT	1128	
QY	1941	TCTCTCTCTCTCACTGAGAGGTGCGGCGGGGGAAGACACACTCTCTTCAAGATGTGACCT	2000	
DB	1129	GACTTTCTCTCCATCATGTGTGCTTCAAGAGATCAACCTTGTCTTGAAGTCAACACT	1188	
QY	2001	GAGGTGCTCATGTGAG 2016		
DB	1189	GAAATATCAATTAA 1204		

RESULT 7

US-08-923-454A-7

Sequence 7, Application US/08923454A

Patent No. 6004794

GENERAL INFORMATION:

APPLICANT: Creasy, Caretha

APPLICANT: LiVi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 251...1624
OTHER INFORMATION:
US-08-923-454A-7

Query Match 9.7%; Score 290.6; DB 3; Length 1835;
Best Local Similarity 57.6%; Pred. No. 4e-60;
Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

1017 CTGGCCCTTCCGCGCAGGCTCTCCACACAGCTAGAGCCCGGCTACAAAGTTCAAC 1076
635 CCGGCGCTCTCGCCGCGCTCTTACCGCGCGCGCTTCTCCCGAGTCAAGTCAAC 694
1077 TTCTATTGTCAGCTGTGTGAAGAAAGATCGACACGCGGTGTTCATATGACTCTTCTG 1136
695 TTCATGCGAGATGTGTGTGAAGAAAGACAGCACTGCGGTGTCTATATCGAGATCCTGAC 754
1137 AAGACACCCGCTGTTTGGCCGCGCAACGTGCCCCCTGTCCAGGGGTTTGGCTTCATCAGTCA 1196
755 CGGACCTCTTTCTTGGGCGCGGAGGTCCCTATCTCGACGGCTCAGGATTCGTGTGGCT 814
1197 GAGGCGGCTGTATCATCAACAAATGCCAGTGTGTCCAGCAAGTGTGCTGCCGCGGC 1256
815 GCGGATGGCTATTGTACCAACGCCCATGTGTG-----GCTGAT 856
1257 AGCGACAGCTCAAGGTGAGCTACAGAAATGGGAGCTCTATGAGGCCCATCAAAAGAC 1316

857 CCGCGCAGAGTCCGTGTGAGACTGCTAAGCGCGCAGACGTATGAGGCCGTGTCAACGT 916
1317 ATCGACAAAGATCGGAGATTGGCCACATCAAGATCAATCCCAAGAAAAGCTCCCTGG 1376
917 GTGATCCCGTGGCAGACATGCAACGCTGAGGATTCAGATTAAGAGCTCTCCCGACG 976
1377 TTGTGCTGGGTCACTCGGCGCAGCTTGGCGCTTGGGAGTTTGTGTGGCCATCGGCACT 1436
977 CTGCTCTGGGACGCTCAGCTGATGTCCGGGAAGGAGTTTGTGTGGCCATGGGAAGT 1036
1437 CCGTTGCCCTTACAGAACAGTGAACAGGCGCATCTGACGACTGCCAGCGGAGGCG 1496
1037 CCGTTGCACTGCAAGAACAGATCAATCCGCGATTTAGTCTGTCTCAGGCTCAGCG 1096
1497 AGGAGCTGGGCTCCGGGACTCCGACATGAGCTCATCCAGACGGATGCCATCAAC 1556
1097 AAGACCTGGGACCTCCCGCAACAAATGTGAATCATTTCAACTGATGACGCTATTGAT 1156
1557 TACGGAACTCCGGGGGACCACTGTGAACTGTGAGCGAGTCAATTGGCATCAACAG 1616
1157 TTGGAACCTGAGAGTCCCTGGTTAACTGATGGGAGGTATTTGAGTGAACAC 1216
1617 CTGAAGTCAAGCTGCGCATCTCTTTGGCATCCCTCAGACCGCATCAAGGTTCTTC 1676
1217 ATGAAGGTCAAGCTGGAATCTCTTGGCATCCCTCTGATCGTCTTGAAGTTTCTG 1276
1677 ACAGAGTCCAAAGACAAAGCA-----GATCAAAAGCTGGAAGAGCGCTTCATC 1724
1277 CATCGTGGGAAAGAAAGAAATTCCTCTCCGGAATCACTGGGTCACAGCGGCTTACAT 1336
1725 GGCATACGAGATGCGGAGATCAACCAAGCTGTGTGATGAGCTGAAGGCCAGCAACCG 1784
1337 GGGGTGATGATGCTACCCCTGATCCAGCATCTTCTGAACTACAGCTTGAAGAACCA 1396
1785 GACTTCCAGAGGTGAGAGTGAATTTATGTGCAAGGTTGCCCGCAATTCACCTTCT 1844
1397 AGCTTCCGATGTTCAGCATGTGTACTCATCTCAATTAAGTATCTGGGCTCCCTGCA 1456
1845 CAGAGAGGCGCATCCAGATGTGATCATCTGTCATGTCAGGTCAGGCGCTCTCTAGTG 1904
1457 CACCGGCTGTCTCTCGGCTGTGTATGTGATTTTGGCCATTGGGAGCAGATGTACAA 1516
1905 GACTGAGTGAAGCTCAGAGAGCCGCTGTGACCGAGTCTCTCTCTACTGAGGTGCGG 1964
1517 AATGCTGAAGATTTTATGAGCTGTTCGAACCCATCCAGTGTGAGTGCAGATCCGG 1576
1965 CCGGGGAACAGACACTCTCTTTCAGCATCGACCTGAGGT 2005
1577 CCGGGACGAGAAACACTGACCTTATATGTGACCCCTGAGGT 1617

RESULT 8
US-09-075-460-4
Sequence 4, Application US/09075460A
Patent No. 6489136
GENERAL INFORMATION:
APPLICANT: Zervos, Antonis S.
TITLE OF INVENTION: CELL PROLIFERATION RELATED GENES
FILE REFERENCE: 10284/004001
CURRENT APPLICATION NUMBER: US/09/075,460A
EARLIER FILING DATE: 1998-05-08
EARLIER APPLICATION NUMBER: US 60/046,077
EARLIER FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (248) ... (1834)
US-09-075-460-4

Query Match 9.7%; Score 290.6; DB 3; Length 2040;
 Best Local Similarity 57.6%; Pred. No. 4.2e-60;
 Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

1017 CTGGCCCTTCCCGCAGGCGAGCTCTCCACAGCTGAGGAGCCCGCGTACAGTTCAAC 1076
 845 CCGGCGCTCTCGCGCGCGTCCCTAGCCCGCGCGCGCTTCTCCCGAGTCAAGTAAAC 904
 1077 TTCAATGCTGAGTGTGAGAAAGATCGACAGCCGTGTCTCACTAGAGCTTTCTCG 1136
 905 TTCAATGAGATGTGTGAGAAAGACAGCACTGCGGTGTCTATATCAAGATCTTGAC 964
 1137 AGACACCGGCTGTTGGCGCAACGTGCCCTGTCCAGGCTTCTGGCTTCAATGTCA 1196
 965 CGGACCCCTTCTTGGCGCGCGAGGCTCCCTATCTGAGAGGCTCAGAGTTCTGTGGCT 1024
 1197 GAGCGCGGCTGATCATCAACATGCCCACTGTGTCTCCAGCAAGTGTGCGCGGCG 1256
 1025 GCGGATGGGCTCATTTGTCAACAGCGCAATGTGTG-----GCTGAT 1066
 1257 AGGCAAGAGCTCAAGTGTCAAGATGGGCACTCTATGAGGCCATCAAGAC 1316
 1067 CGGCGCAGAGTCCGTGTGAGACTGTAGCGGCGACACGTATGAGGCGCTGTGTCAAGCT 1126
 1317 ATCGACAGAAATCGGACATTTGCCCAATCAAGATCCCAAGAAAGCTCCCTGTG 1376
 1127 GTGGATCCCGTGGCAGACATCGCMAAGCTGAGAGATTCAGACTAGAGGCTCTCCCGACG 1186
 1377 TTGTTGCTGGTCACTCGGCGCAGCTGTGCGGAGTTTGTGTGGCCATCGGAGT 1436
 1187 CTGGCTCTGGAGCGCTCAGCTGATGTCCGGCAAGGGAGTTTGTGTGCCATGGGAAGT 1246
 1437 CCCTTGCCCTTACAGAAACAGTGAACAGGGCAATGTGTGACACTGTGCCAGGGAGGCG 1496
 1247 CCTTTGCACTGCAAAACAGTCAATCCGGCAATTTGATGCTGTGAGGCTCAGGCG 1306
 1497 AGGGAGTGGGCTCGGGGACCTCCGACATGAGCTCATCAGAGGATCCATCATCAAC 1556
 1307 AGAGCTGTGGAGCTCCCGCAACCAATGTGAAATTCATCAATGATGAGCTATGAT 1366
 1557 TACGGGAACTCCGGGAGCACTGTGTGAACCTGTAGTGGAGGATCATTTGGCTCAACG 1616
 1367 TTTGGAATCTCGAGGTCCCTGTGTAACTGATGGGAGGTGATTTGATGAAACCC 1426
 1617 CTCAAGTCAAGGCTGTGCTCTTTGCTGCTCCCTCAGACCGCATCAACGTTCTC 1676
 1427 ATGAAGTCAAGCTGGAATCTCTTTGCTGCTCCCTGATGCTTGTGAGAGTTTCTG 1486
 1677 ACAAGATTCAGACAAAGCA-----GATCAAGACTGGAAGAAAGGCTTCAATC 1724
 1487 CATCGTGGGAAAGAAATTCCTCTCCGAAATCAGTGGGTCCAGCGGCTCATATT 1546
 1725 GGCATACGAGTGCAGATCAACCAAGCTGTGTGATGAGCTGAAGGCCAGCAACCG 1784
 1547 GGGGTGATGATCTGACCTGTAGTCCAGCATCTTTGCTGAATCAAGTTTGAAGAAC 1606
 1785 GACTTCCAGAGCTCAGAGTGAATTTATGTGCAAGAGTTTCCGCAATTCACCTTCT 1844
 1607 AGCTTTCCGATGTTCAAGCATGTGTAATCATCAATTAAGTCACTCTGGGCTCCCTGCA 1666
 1845 CAGAAAGGCGCATCCAGATGTGATCATCATGTCAAGTCAAGGCGGTCTCTAGTG 1904
 1667 CACCGGCTGTGTCTGTGGGCTGTGTGATTTGGCCATTGGGAGAGATGTGACAA 1726
 1905 GACTGAGTGAAGTGAAGGCGGTGTGACCGAGTCTCTCTCTCACTGAGAGTGTGCG 1964
 1727 AATGTGAAGATGTTATTAAGCTGTGCAACCAATCCAGTTGGCAATGCAAGATCGG 1786
 1965 CGGAGGAAGCAGACCTCTCTTCAAGCATGCACTGAGGT 2005
 1787 CGGAGCAGAAACACTGACTTATATGTGACCCCTGAGGT 1827

RESULT 9
 US-08-923-454A-23
 ; Sequence 23, Application US/08923454A
 ; Patent No. 6004794
 ; GENERAL INFORMATION:
 ; APPLICANT: Creasy, Caretha
 ; APPLICANT: Liavi, George
 ; APPLICANT: Karian, Eric
 ; APPLICANT: Clinkenbeard, Helen
 ; APPLICANT: Browne, Michael
 ; APPLICANT: Southan, Christopher
 ; TITLE OF INVENTION: HUMAN SERINE PROTEASE
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/923,454A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 60/025436
 ; FILING DATE: 06-SEPT-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Baumeister, Kirk
 ; REGISTRATION NUMBER: 33,833
 ; REFERENCE/DOCKET NUMBER: P50547
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610-270-5096
 ; TELEFAX: 610-270-5090
 ;
 ; INFORMATION FOR SEQ ID NO: 23:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2187 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 603...1976
 ; OTHER INFORMATION:
 ; US-08-923-454A-23

Query Match 9.7%; Score 290.6; DB 3; Length 2187;
 Best Local Similarity 57.6%; Pred. No. 4.3e-60;
 Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

1017 CTGGCCCTTCCCGCAGGCGAGTTCACACAGCTGAGGAGCCCGCGCTACAGTTCAAC 1076
 987 CCGGCGCTCTCGCGCGCGTCCCTAGCCCGCGCGCGCTTCTCCCGAGTCAAGTAAAC 1046
 1077 TTCAATGCTGAGTGTGAGAAAGATCGACAGCCGTGTCTCACTAGAGCTTTCTCG 1136
 1047 TTCAATGAGATGTGTGAGAAAGACAGCACTGCGGTGTCTATATGAGATCTTGAC 1106
 1137 AGACACCGGCTGTTGGCGCAACGTGCCCTGTCTCAGCGGTTTGTGCTTCAATGTCA 1196
 1107 CGGACCCCTTCTTGGCGCGCGAGGCTCCCTATCTGAAAGGCTCAGGATTCGTGTGGCT 1166

QY 1197 GAGCCGCGCTGATCATACCAATGCCAGTGTGTCCAGCAACAGTCTGCCCCGGGC 1256
DB 1167 GCCGATGGCTCATTTGTACCAAGCCCATGTGTG-----GCTGAT 1208
QY 1257 AGGACAGAGCTCAAGGTGACGTACAGATGGGAGCTCTATAGAGCCACCATCAAGAC 1316
DB 1209 CGCGGAGAGTCCGTGTGAGACTGTAAAGGGGAGACGTATAGGCGGTGTGACAGCT 1268
QY 1317 ATGACAAAGATTCGACATTTGCCACATCAAGATTCATCCAAAGAAAAGCTTCCCTG 1376
DB 1269 GTGGATCCCGTGGCAGACATCGAACGCTGAGATTCACTAAAGGAGCTCTCCACAG 1328
QY 1377 TTGTGTGGGTGATCTCGCGGACCTGCGGCTGGGGAGTTTGTGGGCGCATCGGAGT 1436
DB 1329 CTGCTCTGGAGAGCTGATGATGTCGGCAAGGGAGTTTGTGTGCGCATGGAGT 1388
QY 1437 CCCTTGCCCTTACAGAACACAGTGAACACGGGATCGTCAGCATGCGCCAGCGGAGGCG 1496
DB 1389 CCCTTGGCACTGAGAACACAGATCAATCCGGCATTTGTAGCTGTGTGACGCGTCCAGCC 1448
QY 1497 AGGAGTGGGCTCCGGGACTCCGACATGACCTACATCCAGACGATGCTATCAAC 1556
DB 1449 AGGAGCTGGGACTCCCGCAACCAATGTGAAATACATTCMACTGATGCACTATTGAT 1508
QY 1557 TACGGGAATCCGCGGGGACCACTGTGAACTGTGATGGCGAGGTCAATTGGCATCAACG 1616
DB 1509 TTTGGAAATCTGTGAAGTCCCTGTGTTAACTGATGGAGGTGATTTGAGTGAACACC 1568
QY 1617 CTCAGAGTCAAGCTGGCATCTCTTTGGCATCCCTCAGACCGATCAACGGTTCTTC 1676
DB 1569 ATGAAAGTCAAGCTGGAATCTCTTTGGCATCCCTTGTGATGCTCTGAGAGTTTCTG 1628
QY 1677 ACAGATTTCCAAACAAGCA-----GATCAAGACTGGAAGAAAGCCTTCAATC 1724
DB 1629 CATGTGGGGAAAGAAATTCCTCTCGGAATAGTGGGTCCAGGGCGCTCAATT 1688
QY 1725 GGCATACGATGGGAGCATATCACCAAGCTGTGATGAGCTGAAGGCGACGACCGG 1784
DB 1689 GGGGTATGATGCTGACCTGAGTCCACAGATCTCTTGTAACGTGACCTTGAGAACCA 1748
QY 1785 GACTTCCCAAGGTGACAGTGAATTTATGTGCAAGAGTTGCGGCAATTCACCTTCT 1844
DB 1749 AGCTTCCGATGTTGACATGTGTATCATCATTAAGATCACTCGGCTCCCTGCA 1808
QY 1845 CAGAGAGGGGCAATCCAGATGTGTGATCATGTGCAAGTCAAGGGGTCTCTAAGT 1904
DB 1809 CACCGGCTGTGTCTGCGCTGTGTATGTATTTGGCCATTTGGGAGACAGATGTACAA 1868
QY 1905 GACTCAGTGAAGCTGACGAGAGGCGGTGACCGAGTCTCTCTCACTGAGGTGCGG 1964
DB 1869 AATGCTGAAGATTTATGAGCTGTTCGAACCCCAATCCAGTTGGCAATGTGAGATCCG 1928
QY 1965 CGGGGGAAGACGACTCTCTTTCAGCATGCACTGAGGT 2005
DB 1929 CGGGGACGAGAAACACTGACTTATATGTGACCCCTGAGGT 1969

RESULT 10
US-08-923-454A-24
Sequence 24, Application US/08923454A

Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karan, Eric
APPLICANT: Clindenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumleiser, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 603..1976
OTHER INFORMATION:
US-08-923-454A-24
Query Match 9.7%; Score 290.6; DB 3; Length 2187;
Best Local Similarity 57.6%; Pred. No. 4,3e-60;
Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;
QY 1017 CTGCGCTTCCCGCAGCGCAGTCTCCACGACTGACGACCCGCGCTACAGTTCAAC 1076
DB 987 CGCGCCGTCTTCGCGCGCGCTTACGCGCGCGCGCTTCTCCCGAGTCAAGTACAAAC 1046
QY 1077 TTCAATGTGACGTGTGGAAGAATGACACAGCCGCTGTCCATATGAGCTCTTCTG 1136
DB 1047 TTCAATGTGAGATGTGTGAAGAAGACAGACCTGCGGTATATGAGATGATCTGAGC 1106
QY 1137 AGACACCCGCTGTTTGGCCGCAAGTGCCTGTCCAGCGGTTTGTGCTTATCATGTCA 1196
DB 1107 CGGACCCCTTCTTGCGCGGAGAGTCCCTATCTCGAAGGCTCAGAAATTCGTGTGCT 1166
QY 1197 GAGCGCGCTGATCATCAACCAATGCCACGTGTGTCCAGAACAGTGTGCCCCGGGC 1256
DB 1167 GCCGATGGCTCATTTGTACCAAGCCCATGTGTG-----GCTGAT 1208
QY 1257 AGGACAGAGCTCAAGGTGACGTACAGATGGGAGCTCTATAGAGCCACCATCAAGAC 1316
DB 1209 CGCGGAGAGTCCGTGTGAGACTGTAAAGGGGAGACGTATAGGCGGTGTGACAGCT 1268
QY 1317 ATGACAAAGATTCGACATTTGCCACATCAAGATTCATCCAAAGAAAAGCTTCCCTG 1376
DB 1269 GTGGATCCCGTGGCAGACATCGAACGCTGAGATTCACTAAAGGAGCTCTCCACAG 1328
QY 1377 TTGTGTGGGTGATCTCGCGGACCTGCGGCTGGGGAGTTTGTGGGCGCATCGGAGT 1436
DB 1329 CTGCTCTGGAGAGCTGATGATGTCGGCAAGGGAGTTTGTGTGCGCATGGAGT 1388


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QY 1437 CCCTTCCCTCAAGAACAGTGAACAGGCGATCTGACACTCCCAAGCGGAGGCG 1496
DB 1389 CTTTTTGCACTGAGAAACAGATCAATCCGATATTGATGCTCTCAGCGCTCAAGCC 1448
QY 1497 AGGAGCTGGGCTCCGGGACTCCGATGACATGACATCAACAGCGATCCATCATC 1556
DB 1449 AGAGACTGGGACTCCCGCAACCAATGAGAAATACATTCAATCTATGATTTGAT 1508
QY 1557 TACGGAACTCCGGGGACCACTGTGAACTTGGATGCGAGGTCATTGGCATCAAC 1616
DB 1509 TTTGGAACCTTGAGAGTCCCTGTTAACTGGATGGGAGGTGATGAGTGAACACC 1568
QY 1617 CTCGAAGTCAAGCGCTGGCATTTCTTTGCTGATCTCCCTCAGACCGCATCAACG 1676
DB 1569 ATGAAGTCAAGCTGGAAATCTCTTTCATCTCCCTTGTGATCTTCTGAGAGTTCTG 1628
QY 1677 ACAGAGTCCAGAACAGCA-----GATCAAGACTGGAAGAGCGCTTCATC 1724
DB 1629 CATCGTGGGAAAGAAAGAAATTCCTCTCCGAAATAGTGGTCCAGCGGCGCTACAT 1688
QY 1725 GGCATACGATGCGAGCATCAACCAAGCTGTGGATGAGCTGAAGGCCAGCAACCG 1784
DB 1689 GGGGTATGATGCTGACCTGAGTCCAGCATCTTGTGACTACAGCTTGAGAACCA 1748
QY 1785 GACTTCCAGAGTCAAGCTGAAATTTATGTCAGAGAGTGGCGCAATTCACCTTCT 1844
DB 1749 AGCTTTCCGATGTTTACGATGTTATCATCAATCAATCAATCTGAGCTCCCTGCA 1808
QY 1845 CAGAGAGCGGATCCAGATGTTGATCATCTGCAAGTCAAGCGGCGCTCTGATG 1904
DB 1809 CACCGGCTGTGCTGCGCTGATGATGATTTGGCAATGGGAGAGATGTTACAA 1868
QY 1905 GACTGAGTGAAGTGAAGAGCGCTGTCAGAGTCTCTCTCTGAGAGTGGCG 1964
DB 1869 AATGCTGAAGATGTTATGAGCTGTTCAACCAATCCAGTTGCAAGTGAAGTCCGG 1928
QY 1965 CCGGGGAACGAGCACTCTCTTTCAGCATGCACTGAGGT 2005
DB 1929 CCGGAGCAGAAACATGACCTTATATGAGCCCTGAGGT 1969

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RESULT 11

US-09-008-271A-23

Sequence 23, Application US/09008271A

Patent No. 6203979

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

Hillman, Jennifer L.

Yue, Henry

Guegler, Karl J.

Corley, Neil C.

Tang, Tom Y.

Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271A

FILING DATE: 16-Jan-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>

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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDBESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINDUCT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 23 :
US-09-008-271A-23

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Query Match 9.7%; Score 290.6; DB 3; Length 2476;

Best Local Similarity 57.6%; Pred. No. 4,5e-60;

Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

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QY 1017 CTGGCCCTTCCCGGAGGAGTCTCCACAGCTGACAGCGCGGCTACAGTTCAAC 1076
DB 445 CCGGCGCTCTGCGCGCTGAGCCCGCGCGCGCTTCTCCCGAGTCAATCAAC 504
QY 1077 TTTATTTGTCAGTGTGAGAGATTCGACAGCGGCTGTCACATGAGCTTCTCTG 1136
DB 505 TTTCATGCAAGTGTGTGAGAGAGACAGCAGCTGCGGTGCTATATGAGATTCCTGAGC 564
QY 1137 AGACAACCGCTGTTGGCGCAACGTCCTGTCAGAGGTTGCTTCAATGTCAT 1196
DB 565 CCGCACCTTTCTTGGCGCGAGAGTCTCTATCTGAAACGCTCAGAGATTGCTGAGCT 624
QY 1197 GAGCGCGCTGATATATCAACCAATGCCAGTGTGTCAAGAACAGTGTGCGCGGCG 1256
DB 625 GCGATGAGCTCATTTGTACCAACGCCCATGTTGTTGTTGTTGTTGTTGTTGTTGTT 666
QY 1257 AGGCAAGCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1316
DB 667 CCGGCAAGTCCGTTGAGAGTCTGTAAGCGGCGAGAGTGAAGCGGTGTCACAGCT 726
QY 1317 ATGCAAGAGTGGAGCATTTGCAATCAATCAATCAATCAATCAATCAATCAATCA 1376
DB 727 GTGATCTCCGTTGGCAGATGCGCAACGCTGAGATTTCAAGTCAAGAGCTTCCCA 786
QY 1377 TTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1436
DB 787 CTGCTCTGAGAGCTGCTGAGCTGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 846
QY 1437 CCCTTCCGCTCAGAACAGTGAACAGGAGCATCTGACAGCTGCCAGCGGAGGCG 1496
DB 847 CCGTTTGAAGTCAAGAACAGTCAATCAATCCGAGTTTGAAGTCTGCTGCTGCTGCTG 906
QY 1497 AGGAGCTGGGCTCCGGGACTCCGATGATGATCAATCAATCAATCAATCAATCAAT 1556
DB 907 AGAGACTGGGAGCTCCCAACCAATGATGATGATGATGATGATGATGATGATGATGAT 966
QY 1557 TACGGAACTCCGGGGACCACTGTGAACTTGTGATGCGAGTCAATGAGTCAACAG 1616
DB 967 TTTGGAACCTTGAGAGTCCCTGTGTAACCTGAGTGGAGAGTATTGAGTGAACACC 1026
QY 1617 CTCGAAGTCAAGGCTGATCTCTTTGCTGATCTCCCTCAGACCGCATCAACAGTTCTC 1676
DB 1027 ATGAAGTCAAGCTGAGATCTCTTTGCTGATCTCCCTTGTGATGCTTGTGAGAGTT 1086
QY 1677 ACAGAGTCCAGAACAGCA-----GATCAAGACTGGAAGAGCGCTTCATC 1724
DB 1087 CATCGTGGGAAAGAAAGAAATTCCTCTCCGAAATCAATGAGGTCCACGCGGCTACAT 1146
QY 1725 GGCATACGAGTCCGAGCATCAACCAAGCTGTGATGAGCTGAAGGCCAGCAACCG 1784

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Db 1147 GGGGTATATATGCTGACCTCGATGCCAGATCCTTGCTGAATCAAGCTTGCAGAACCA 1206
Qy 1785 GACTTCCCAAGAGTCAAGACATGGAATTTATGTGCAAGAGTTGCGCGAATTCACCTTCT 1844
Db 1207 AGCTTCCCATATGTCAGATGTTGTATCATCATTAAGATGATCTCTGGGCTCCCTGCA 1266
Qy 1845 CAGAGAGGGGAGTCAAGATGTTGATCATGATGTCAGAGTCAAGGGGCTCTCTAGTG 1904
Db 1267 CACGGGCTGTCTGCGGCTGTGATGATTTTGGCCATTTGGGAGCAGATGTACAA 1326
Qy 1905 GACTCGAGTGAAGTGAAGAGAGCGGTGCTGACCGAGTCTCTCTACTGAGAGTGGC 1964
Db 1327 AATGCTGAAGATTTTATGAAAGCTGTTCGAACCCATTCAGTTGGCAGATGCAATCCG 1386
Qy 1965 CGGGGGAACGACGACCTCTCTTTCAGCAGTCACTGAGGT 2005
Db 1387 CGGGAGAGAAACACTGACCTTATATGTGACCCCTGAGGT 1427

RESULT 12

US-09-968-415-23
Sequence 23, Application US/09968415
Patent No. 6855811
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,415
FILING DATE: 26-Sep-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/659,151
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINICT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 23 :
US-09-968-415-23

Query Match 9.7%; Score 290.6; DB 3; Length 2476;
Best Local Similarity 57.6%; Pred. No. 4.5e-60;

Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;
Qy 1017 CTGGCCCTTCCCGCAGCGCAGGTCTCCACCAAGCTGAGAGCCGCGCTTCAAGTTCAAC 1076
Db 445 CCGGCGGCTCTCCCGCGCGCTCCCTAGCCCGCGCGCGCTTCTCCCGAGTCAAGTACAA 504
Qy 1077 TTCAATGTCAGAGTGTGAGAGATTCGACCAAGCGGTGTCACATGATGAGCTTCCG 1136
Db 505 TTCAATGTCAGATGTGTGAGAGAGACAGACCTGCGGTGTATATGAGATCTTGAC 564
Qy 1137 AGACACCCGCTGTTGGCGCAACGTGCGCTGTCCAGCGGTTCGCTTCAATGTCA 1196
Db 565 CCGGACCCCTTTCTTGGGCGGAGGTCCCTATCTCGAAGGTGAGATTTGGTGGCT 624
Qy 1197 GAGCGGCGCTGATATATCAACCAATGCCAGTGTGTCCAGCACAGTGTGCCCCGGC 1256
Db 625 GCCGATGGGCTCATTTGTACCAACGCCCATGTGGTG-----GCTGAT 666
Qy 1257 AGGCAGAGCTCAAGTGCAGCTACAGAAATGGGGCTCTATGAGGCCACCATCAAAAGAC 1316
Db 667 CCGCGCAGAGTCCGTGTAGACTGTAAAGCGGCGACAGTATGAGGCCGTGTACAGCT 726
Qy 1317 ATGCACAAGATCGGACATTTGCCACATCAAGATCCATCCCAAGAAAAGCTCCGTG 1376
Db 727 GTGATCCCGTGGGAGACATCGCAACGCTGAGGATTCAGACTTAAGAGACCTTCCCAAG 786
Qy 1377 TTGTGCTGGGTCACTCGGCGGACCTGGGCGCTGGGAGTTTGTGTGATCGGAGT 1436
Db 787 CTGCTCTGGGACGCTCAGCTGATGTCCGGAGAGGGGAGTTGTGTGGCCATGGGAAGT 846
Qy 1437 CCCTTGCCCTTACAGAACACAGTGAACAAGGAGATCGCAGACCTGCCAGCGGAGGGC 1496
Db 847 CCTTTGACATGCAAGAACACATCAATCCGACATTTAGCTGTGCTCAGCGTCAAGCC 906
Qy 1497 AAGGAGCTGGGCTCCCGGAGCTCCGACATGAGTCAATCCAGACGATGCCATCAAC 1556
Db 907 AGAGACTGGGAGCTCCCGCAACCAATGTGAATACATTAACATGATGAGTATGAT 966
Qy 1557 TAAGGAACTCCGGGGGACACTGTGTAACTGTGATGCGAGTTCATTTGATCAACAG 1616
Db 967 TTTGGAACCTCTGGAGGTCCCTGTGTAACTGTGATGAGGAGGTGATGAGTAAACCC 1026
Qy 1617 CTAAAGTCAAGGCTGCGATCTCTTTGSCATCCCTCAGACCGCATCAACGGTTCTC 1676
Db 1027 ATGAAGTCAAGCTGGAATCTCTTTGCCATCCCTTGTATGCTTTCCAGAGTTTGTG 1086
Qy 1677 ACAAGTTCAGACAGCA-----GATCAAAAGCTGGAAGAGCGTTTCATC 1724
Db 1087 CATCGTGGGAAAGAAAGAAATTCTCTCCGGAATCAAGTGGGTCCAGCGGCGCTACAT 1146
Qy 1725 GGCATACGAGATGCGGAGCATCAACCAAGCCTGTGTGATGCTGAAAGGCCAGAACCCG 1784
Db 1147 GGGGTGATGATGCTGACCTGATGCCAGCATCTTGTGAACATCAAGCTTTCGAGAACCA 1206
Qy 1785 GACTTCCCAAGAGTCAAGAGTAAATTTATGTGCAAGAGTTGGCGCAATTCACCTTCT 1844
Db 1207 AGCTTCCCATGTTTCAAGATGTGTACTCATCAATAAGTCAATCTCGGCTCCCTGCA 1266
Qy 1845 CAGAGAGCGGCATCCAAAGATGTGATCATCTGTCAAGGTCAACGGGCGTCTCTAGTG 1904
Db 1267 CACGGGCTGTCTGCGGCTGTGTGATGATTTTGGCCATTTGGGAGCAGATGTACAA 1326
Qy 1905 GACTCGATGAGCTGCAAGAGCCGTGTGACCGAGTCTCTCTCTACTGAGAGTGGC 1964
Db 1327 AATGCTGAAGATGTTTATGAAGCTGTTCGAACCCAAATCCAGTTGGCAGTGCAGATCCG 1386
Qy 1965 CGGGGGAACGACGACCTCTCTTCAAGATCGCAGCTTGAAGT 2005
Db 1387 CGGGAGAGAAACACTGACCTTATATGTGACCCCTGAGGT 1427

RESULT 13

US-08-923-454A-30

Sequence 30, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE: Polymorphic variants at 672 and 1435
NAME/KEY: aa24=Arg/Cys aa278=Ala/Val
LOCATION: 603...1976
OTHER INFORMATION:
US-08-923-454A-30

Query Match 9.6%; Score 289; DB 3; Length 2187;
Best Local Similarity 57.5%; Pred. No. 1e-59;
Matches 576; Conservative 0; Mismatches 395; Indels 30; Gaps 2;

QY 1017 CTGGCCCTTCCGCGAGGCTGTCACGAGCTGAGAGCCGCGCTTCAAGTTCAAC 1076
DB 987 CCGGCGCTCTCGCGCGCTCCCTTACCCCGCGCGCTTCTCCCGAGTCAATCAAC 1046
QY 1077 TTCAATGCTGAGCTGTGTGAGAGATCGACAGCCGTGTCCACATAGACTTTCTCG 1136
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DB 1107 CGGACCCCTTCTTGTGGCGCGAGGCTCTTATCTCGAAGGCTTGTGTGCTGTGCT 1166
QY 1197 GAGGCGGCTGATCATCAATGCGCAGTGTGTGTCCAGCAAGTGTCTGCCCCGGGC 1256

DB 1167 GCGAATGGGCTCATTTGTACCAAGCCCATGTGGTG-----GCTGAT 1208
QY 1257 AGGACAGCTCTAAGTGTGACAGTACAGATGGGAGCTCTTATAGGCCACCATCAAGAC 1316
DB 1209 CGGCGCAGAGTCCGTGTGAGCTGTAAAGCGCGACAGTATGAGCGGTGTGACACT 1268
QY 1317 ATCGAAGAAGTGGGAGATTGGCCACATCAAGATCCATCCCAAGAAAAGCTCCCTGTG 1376
DB 1269 GTGATCCCGTGGCAGACATGCAACGCTGAGATTGAGATTGAGAGACCTTCCCAAG 1328
QY 1377 TTGTTGCTGGGTCACTCCGCGAGCTGTGCGGCTGGGAGTTGTGTGGCCATCGGAGT 1436
DB 1329 CTGCTCTGGAGACGTGACGTGATGTGTCCGGAGGGAGTTGTGTGTGTCATGGAGT 1388
QY 1437 CCTTGTGCTTACAGACAGTGAACAAGGAGATGTCAGACCTGCCAGCGGAGGAGGC 1496
DB 1389 CCTTGTGCTGACAGAACAGATCAATCCGAGATTGTAGCTCTCTCTCAGGCTCAGGC 1448
QY 1497 AGGAGCTGGGCTTCCGCGAGCTCCGACATGAGACTACATCCAGAGGATGCCATCAAC 1556
DB 1449 AGAGACTGGAGCTCCCGCAACAGATGTGAATATTCATAATGATGACGCTATTGAT 1508
QY 1557 TACGGAACTCCGGGGAGCACTGGTGAACCTGTGATGCGAGTCAATGGCATCAACAG 1616
DB 1509 TTTGGAATCTGGAAGTCCCTGTGTAACTGTGATGGGAGGTGATTGGAGTGAACAC 1568
QY 1617 CTCAAGTCAAGCTGTGATCTCTTTGCCATCCCTTCAAGACCGCATCAACGGTTCTC 1676
DB 1569 ATGAAGGTCAAGCTGTGAATCTCTTTGCCATCCCTTGTGAATGCTTGTGAGAGTTCTG 1628
QY 1677 ACAAGTTCGAAGCAACA-----GATCAAGACTGGAAGAGGCTTCATC 1724
DB 1629 CATGCTGGGAAAGAAAGAAATTTCTCTCCGAAATCAATGGGTCCACGGGCTTACTT 1688
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DB 1689 GGGGTGATGATGTGACCTGATGCCAGCATCTGTGTAAGTCAAGCTTGCAGAACCA 1748
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DB 1749 AGCTTCCGATGTCAAGATGTGTACTCATTCATAAGTCAATCTGGGCTCCCTGCA 1808
QY 1845 CAGAGAGCGGCTATCAAGATGTGTGATCATTCGCAAGTCAACGGGCTCTCTAGTG 1904
DB 1809 CACGCGGTGTGTGCGGCTGTGTGTATTTGSCCATTTGGGAGCAAGTGTACAA 1868
QY 1905 GACTGAGTGAAGTCAAGAGGCGGTGTGACCGAGTCTCTCTCTTACTGAGGTGCGG 1964
DB 1869 AATGCTGAAGATGTTATGAAGCTGTGAAACCCAAATCCAGTTGCGAGTGTGAGATCCGG 1928
QY 1965 CGGGGAAAGCAAGACTTCTTTGAGATCGCACTGAGT 2005
DB 1929 CGGGGACGAGAAACACTGACCTTATATGTGACCCCTGAGT 1969

RESULT 14
US-08-322-742-18
Sequence 18, Application US/08322742
Patent No. 568641
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: CANCER DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb


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QY 1317 ATCGACAAGAGTCGGAACCTTCCACCATCAGATCCATCCCAAGAAAAAGCTCCCTGTC 1376
Db 628 GTGGATCCCGTGCGACAGATCCCAACGCTGAGGAAATTCAGACTAAGAGCTCTCCCCACG 687
QY 1377 TGTGCTGAGGTCACTCGGCGGACCTGCGGAGTTGTGTGCGCATCGGAGT 1436
Db 688 CTGCTCTGGACGCTCAGCTGATGTCCGGCAAGGGAGTTGTGTGCGCATGGGAGT 747
QY 1437 CCTTCGCTTACAGAACACAGTGAACAACGGGCATGTCAGCACTGCCAGCGGAGGCG 1496
Db 748 CCTTGGCACTGACAGAACAGATCAATCCGGCATGTGACTCTGCTCAGCGTCCAGCC 807
QY 1497 AAGGAGCTGGGCTCCGGGACTCCGACATGACATACATCCAGACGGATGCCATCATCAAC 1556
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QY 1557 TACGGGAACCTCCGGGGGACCACTGTGTAACCT----- 1588
Db 868 TTGGAAACTCTGAGAGTCCCTGTGTAACCTGCTAGGGAACCTGGGGGCTGTATCCCTG 927
QY 1589 --GGAATGGAGGTCAATTGGCATCAACAGCTCAAGGTCAAGGCTGGCATCTTTGCC 1646
Db 928 CAGGATGGGAGGTGATTTGAGTGAACACCATGAAGTCAAGCTGGAATCTCTTTGCC 987
QY 1647 ATCCCTCAGACCGCATCAACGTTCTT 1675
Db 988 ATCCCTTGTATGTCCTTCGAGAGTTCT 1016
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OM nucleic - nucleic search, using sw model

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(without alignments)
10850.175 Million cell updates/sec

Title: US-10-617-443B-1
Perfect score: 3006
Sequence: 1 caggagactgcaggttcgag.....gccaaaaaaaaaaaaaaaa 3006

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA Main:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3006	100.0	3006	US-10-189-099A-1	Sequence 1, Appli
2	3006	100.0	3006	US-10-617-443B-1	Sequence 1, Appli
3	1962.2	65.3	2543	US-10-485-313A-31	Sequence 31, Appl
4	1953	65.0	2541	US-10-956-157-5181	Sequence 5181, Ap
5	1949.4	64.9	2040	US-09-818-143-14	Sequence 14, Appl
6	1942.8	64.6	2576	US-09-796-753-31	Sequence 31, Appl
7	1813.8	60.3	1868	US-09-764-898-112	Sequence 112, App
8	1783	59.3	2551	US-10-301-822-78	Sequence 78, Appl
9	1472	49.0	2094	US-10-381-820A-7	Sequence 7, Appli
10	1400	46.6	1400	US-10-956-157-10416	Sequence 10416, A
11	1233	41.0	1797	US-10-275-505-28	Sequence 28, Appl
12	1233	41.0	1797	US-11-140-224-28	Sequence 28, Appl
13	1005.4	33.4	1563	US-09-796-753-33	Sequence 33, Appl
14	975	32.4	1044	US-09-796-858-9	Sequence 9, Appli
15	825.2	27.5	2450	US-10-485-313A-26	Sequence 26, Appl
16	667.4	22.2	1695	US-09-969-384-7	Sequence 7, Appli
17	667.4	22.2	1953	US-10-485-313A-32	Sequence 32, Appl
18	666.6	22.2	1788	US-09-764-898-40	Sequence 40, Appl
19	548.8	18.3	1897	US-10-485-313A-38	Sequence 38, Appl
20	495.6	16.5	1328	US-10-764-420-1506	Sequence 1506, Ap
21	457	15.2	457	US-10-485-313A-55	Sequence 55, Appl
22	432.8	14.4	781	US-10-485-313A-48	Sequence 48, Appl
23	396	13.2	396	US-10-485-313A-50	Sequence 50, Appl

24	385	12.8	1440	3	US-09-796-858-7	Sequence 7, Appli
25	385	12.8	1894	6	US-10-104-047-795	Sequence 795, App
26	385	12.8	2034	6	US-10-102-524-1732	Sequence 1732, Ap
27	385	12.8	2036	3	US-09-960-706-516	Sequence 516, App
28	385	12.8	2036	6	US-10-170-385-356	Sequence 356, App
29	385	12.8	2036	6	US-10-172-118-815	Sequence 815, App
30	385	12.8	2036	7	US-10-342-887-815	Sequence 815, App
31	385	12.8	2036	7	US-10-772-636-47	Sequence 47, Appl
32	385	12.8	2036	9	US-10-956-157-919	Sequence 919, App
33	385	12.8	2054	5	US-10-084-817-32	Sequence 32, Appl
34	385	12.8	2437	5	US-10-198-846-10826	Sequence 10826, A
35	384	12.8	2157	6	US-10-264-049-135	Sequence 135, App
36	376.2	12.5	1855	3	US-09-925-298-134	Sequence 134, App
37	376.2	12.5	1855	5	US-10-102-806-134	Sequence 134, App
38	368.4	12.3	619	7	US-10-240-425-73	Sequence 73, Appl
39	368	12.2	2212	8	US-10-723-860-5299	Sequence 5299, Ap
40	346	11.5	1534	3	US-09-765-231A-20	Sequence 20, Appl
41	322.8	10.7	1859	3	US-09-866-050A-588	Sequence 588, App
42	322.8	10.7	1859	3	US-10-152-661-588	Sequence 588, App
43	300.6	10.0	1544	8	US-10-789-241-49	Sequence 49, Appl
44	300.6	10.0	1544	8	US-10-772-636-7	Sequence 7, Appli
45	300.6	10.0	1553	3	US-09-935-350A-18	Sequence 18, Appl

ALIGNMENTS

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RESULT 1
US-10-189-099A-1
; Sequence 1, Application US/10189099A
; Publication No. US20040005659A1
GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Cailin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/189,099A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: cDNA
; ORGANISM: Homo sapiens
US-10-189-099A-1

Query Match      100.0%; Score 3006; DB 6; Length 3006;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3006; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 CAGGACTCGAAGTTTGCAGTCTTCACACTCAGTTCCACAGATGTGTAGAGGGCAT 60

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      |||
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QY      241 TGTGTGGAATCGAGAGAGCCCGGACAGAGGCCCTGTGCGAGGAACCCCGAGGCTGTAGGC 300
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OY	361	GCAGCAGAAATCTGAGCCCGGGAAAGGGTCCAGGGAAGTTCTGTAACATCTAGCAAGTCG	420
Db	361	GCAGCAGAAATCTGAGCCCGGGAAAGGGTCCAGGGAAGTTCTGTAACATCTAGCAAGTCG	420
OY	421	GGCTGGGGTGTGGCCAAAGTTAGAACAAGATGTAAGGCCCTGTGGACTCAGAAATTTGGCAG	480
Db	421	GGCTGGGGTGTGGCCAAAGTTAGAACAAGATGTAAGGCCCTGTGGACTCAGAAATTTGGCAG	480
OY	481	CTCTTTTGGCCCAAGAGGGGCAAGCTGTGTCCGGGCTTGGGTAGCTCAGAAAGGTCACT	540
Db	481	CTCTTTTGGCCCAAGAGGGGCAAGCTGTGTCCGGGCTTGGGTAGCTCAGAAAGGTCACT	540
OY	541	GGGGGCTTTCACATAACCCCGCCTGGACACTGCTGTAGCCCCCAGGGCTCGAGGGAGCC	600
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OY	601	AGCTGAGGCCATAGAGAGAGGGCCAGTTCTCTCTGTAAAGGATTTGCTGTAGCATGAG	660
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OY	661	GGAAACAGACAGAGGCCCAAGGGGGACTAACCCGAAATCCAGATCCCGGCTCACTCCGTGTG	720
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OY	721	GCTCAGGGCAATATCCTTAACTCTCTGTAGCCTCTGACCAGCCTTAGCAGGGTCCAGTG	780
Db	721	GCTCAGGGCAATATCCTTAACTCTCTGTAGCCTCTGACCAGCCTTAGCAGGGTCCAGTG	780
OY	781	AGGGGGGTGAGGAAGCCACAGCAGTGGAAAGCCTTTTAAACATTCTCGGGGTGAGCGAGC	840
Db	781	AGGGGGGTGAGGAAGCCACAGCAGTGGAAAGCCTTTTAAACATTCTCGGGGTGAGCGAGC	840
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Db	841	CCCTTTCCAAATGCTCTGTGTCTACCTGCACTGCTGTGTAGGGGGTCCCAACGGGCTTC	900
OY	901	AGTGTGGGCTGAGAGCTGAGCTCTGAACTGGGACAAGGGGTCTCAGGAAGAGCTCTCTCC	960
Db	901	AGTGTGGGCTGAGAGCTGAGCTCTGAACTGGGACAAGGGGTCTCAGGAAGAGCTCTCTCC	960
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Db	961	TGCCCACTGGGGATAGGGCTCTGGGAGCTGGGAGCATGTGATCTCAGTAGCACTGG	1020
OY	1021	CCCTTTCGGCCAGCGCAGGTCTTCACACAGCTGAGCAGCCCGGCTTCAAGTTCACTTCA	1080
Db	1021	CCCTTTCGGCCAGCGCAGGTCTTCACACAGCTGAGCAGCCCGGCTTCAAGTTCACTTCA	1080
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Db	1081	TTGCTGACGTGGTGGAGAAAGATCGACAAGCGGTGTCCACATAGAGCTCTTCTGAGAC	1140
OY	1141	ACCGGCTGTTTGGCCGCAACGTGCCCCCTGTCCAGCGGTTCTGGCTTCACTATGTACAGG	1200
Db	1141	ACCGGCTGTTTGGCCGCAACGTGCCCCCTGTCCAGCGGTTCTGGCTTCACTATGTACAGG	1200
OY	1201	CCGGGCTGATCATCAACAAATGCCCCAGTGTGTCCAGCAACAGTGTGCCCCGGGACAGCG	1260
Db	1201	CCGGGCTGATCATCAACAAATGCCCCAGTGTGTCCAGCAACAGTGTGCCCCGGGACAGCG	1260
OY	1261	AGCAGCTCAAGGTGACGTACAGAAATGGGGACACTCTAATAGGCGACATCAAAAGACATGG	1320
Db	1261	AGCAGCTCAAGGTGACGTACAGAAATGGGGACACTCTAATAGGCGACATCAAAAGACATGG	1320
OY	1321	ACAAAGATCGACATTGGCCACCATCAAGATCATCTCCAAAGAAAAGCTCCCTGTGTGT	1380
Db	1321	ACAAAGATCGACATTGGCCACCATCAAGATCATCTCCAAAGAAAAGCTCCCTGTGTGT	1380
OY	1381	TGCTGGGTCACTCGGCGACCTGCGGCTGGGGAGTTTGTGTGTGCTCATCGGACGTCCCT	1440
Db	1381	TGCTGGGTCACTCGGCGACCTGCGGCTGGGGAGTTTGTGTGTGCTCATCGGACGTCCCT	1440

Db	1361	TGCTGGGCTCACTCGGCGGACCTGCGGCGCTGGGAGATTGTGGGTGGCCATCGGCACTCCCT	144C
OY	1441	TCGGCCCTACAAACAAGTGAACAACGGGCACTGTCAGCACTGGCCAGCGGAGGCGAGG	1500
Db	1441	TCGGCCCTACAAACAAGTGAACAACGGGCACTGTCAGCACTGGCCAGCGGAGGCGAGG	1500
OY	1501	AGCTGGGCTTCGGGAGCTCCGACATGAGCTACATCAGACGGAATGCCATCATCAACTACG	1566
Db	1501	AGCTGGGCTTCGGGAGCTCCGACATGAGCTACATCAGACGGAATGCCATCATCAACTACG	1566
OY	1561	GGAACTCCGGGGGACCACTGGTGAAACCTGGATGCGAGGTATTTGGGATCAACACGCTCA	1622
Db	1561	GGAACTCCGGGGGACCACTGGTGAAACCTGGATGCGAGGTATTTGGGATCAACACGCTCA	1622
OY	1621	AGGTCAACGGCTGGGATCTCTTTGGCAATCCCTCGAGACCGGATCAACGATTCCTCAG	1680
Db	1621	AGGTCAACGGCTGGGATCTCTTTGGCAATCCCTCGAGACCGGATCAACGATTCCTCAG	1680
OY	1661	AGTTTCAAAGACAGCATCAAGAATCTGGAAAGACGCTTCATCGGCATACGATGCGGA	1740
Db	1661	AGTTTCAAAGACAGCATCAAGAATCTGGAAAGACGCTTCATCGGCATACGATGCGGA	1740
OY	1741	CGATTCACCAACGCGCTGTGTGATAGAGCTGAAGGCGACGAACCCGGGACTTTCCCAAGCTCA	1800
Db	1741	CGATTCACCAACGCGCTGTGTGATAGAGCTGAAGGCGACGAACCCGGGACTTTCCCAAGCTCA	1800
OY	1801	GCACTGGAATTTATGTGCAAGAGGTGGCGCGAATTCACCTTCTCAGAGAGCGGCACTC	1866
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OY	1861	AAGATGTGACATCATCGTCAAGGTCAACGGGCGTCTTATGTGAACTCGAGTAGCTGC	1920
Db	1861	AAGATGTGACATCATCGTCAAGGTCAACGGGCGTCTTATGTGAACTCGAGTAGCTGC	1920
OY	1921	AGGAGCGCTGTCTGAACGAGTCTCTCTCTCACTGAGAGTCCGGCGGGGAGCAACGACAC	1986
Db	1921	AGGAGCGCTGTCTGAACGAGTCTCTCTCTCACTGAGAGTCCGGCGGGGAGCAACGACAC	1986
OY	1981	TCCTCTTCAGCATGCAACCTGAGGTGTGATGTAGAGGGCGCATTTCTCCACGCGCCAGAC	2048
Db	1981	TCCTCTTCAGCATGCAACCTGAGGTGTGATGTAGAGGGCGCATTTCTCCACGCGCCAGAC	2048
OY	2041	GTCAAGCGCTGCAGACAAACGAGGGGCAAGCGCCCCCGAGATCAAGACGAGACACCG	2100
Db	2041	GTCAAGCGCTGCAGACAAACGAGGGGCAAGCGCCCCCGAGATCAAGACGAGACACCG	2100
OY	2101	TCGGTCTCTCAGACAGGGCGGACGCTCTCTCTGTGTGTCGGGGGACAGCGGAGCTGGG	2166
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OY	2161	TTGGCCAGGGGCGCGAATTTCCGCGCTGGGGAGTGTGGATCAACATCCCGGTGCGGGGA	2220
Db	2161	TTGGCCAGGGGCGCGAATTTCCGCGCTGGGGAGTGTGGATCAACATCCCGGTGCGGGGA	2220
OY	2221	GGGAGGCCCAACATCCCTCTGTAGATGATCTGAAAGTCACTTCCAGATTTCTCCGAT	2280
Db	2221	GGGAGGCCCAACATCCCTCTGTAGATGATCTGAAAGTCACTTCCAGATTTCTCCGAT	2280
OY	2281	ATTTCACAAACTGCTCTTCATGAGAGTCCCTCTCTCTCAAGCTTCCGCTCTGCCCCCT	2340
Db	2281	ATTTCACAAACTGCTCTTCATGAGAGTCCCTCTCTCTCAAGCTTCCGCTCTGCCCCCT	2340
OY	2341	GTGAACACCCATCTGCAAGTATCCCTGCTGCTGCGCCCTCACTGCAAGGTCTGGAGTCC	2400
Db	2341	GTGAACACCCATCTGCAAGTATCCCTGCTGCTGCGCCCTCACTGCAAGGTCTGGAGTCC	2400
OY	2401	AAGCTTCTTCCCTCCCTGACAAACGCGCCACCTGAACCTGAGGCGCCAGCTTCCCTCTG	2466
Db	2401	AAGCTTCTTCCCTCCCTGACAAACGCGCCACCTGAACCTGAGGCGCCAGCTTCCCTCTG	2466
OY	2461	AGGACTTACCAAGCTGTAGGGGCGAGGGCTGTGCTGCTGCAAGCTTGGGGTCTCTGAGGAC	2520
Db	2461	AGGACTTACCAAGCTGTAGGGGCGAGGGCTGTGCTGCTGCAAGCTTGGGGTCTCTGAGGAC	2520

QY 2521 AGGTCAATCTGATCCCTTTGGGGGTGGGGGTCCAGCCAGAGCAGGCACTGAG 2580
DB 2521 AGGTCAATCTGATCCCTTTGGGGGTGGGGGTCCAGCCAGAGCAGGCACTGAG 2580
QY 2581 TGAATGCCCTTGCTGGGAGCTGAGCCCGCTGCA TGAAGTTTCTCCCAAGC 2640
DB 2581 TGAATGCCCTTGCTGGGAGCTGAGCCCGCTGCA TGAAGTTTCTCCCAAGC 2640
QY 2641 AGGCAAGAGCGCGGGGAGCAGTGAAGTTGGCTGCTGCTGGGAACTTCTCTC 2700
DB 2641 AGGCAAGAGCGCGGGGAGCAGTGAAGTTGGCTGCTGCTGGGAACTTCTCTC 2700
QY 2701 CCCAAGGGGCGCATGGGGAGCTGAGAGGAGCAGTGAAGTGGAGCTGGGGGTGAG 2760
DB 2701 CCCAAGGGGCGCATGGGGAGCTGAGAGGAGCAGTGAAGTGGAGCTGGGGGTGAG 2760
QY 2761 GACTGAGCGGCTTCCCTTCCAGCAGCTCTGGGATGACAGCCGCTCGCATGAG 2820
DB 2761 GACTGAGCGGCTTCCCTTCCAGCAGCTCTGGGATGACAGCCGCTCGCATGAG 2820
QY 2821 TGCCGCCAGAGGCAATGAGCTGCTGGGCAACCCCTCATCCAGGGAAGAGTGT 2880
DB 2821 TGCCGCCAGAGGCAATGAGCTGCTGGGCAACCCCTCATCCAGGGAAGAGTGT 2880
QY 2881 CTCAAGGGGCAATTTGAGCTTTGCTGAATGGAATCCAGTTGCTTGAATGTA 2940
DB 2881 CTCAAGGGGCAATTTGAGCTTTGCTGAATGGAATCCAGTTGCTTGAATGTA 2940
QY 2941 TTTCTCTACTGATGGAATAAAGTTTACAAGCACAAGGTTCTCAGCCAAAATAA 3000
DB 2941 TTTCTCTACTGATGGAATAAAGTTTACAAGCACAAGGTTCTCAGCCAAAATAA 3000
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DB 3001 AAAAAA 3006

RESULT 2
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; Sequence 1, Application US/10617443B
; Publication No. US20050019777A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Gailin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/617,443B
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-617-443B-1

Query Match 100.0%; Score 3006; DB 8; Length 3006;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3006; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 TGTGGGAATCTGAGAGAGCCCGGAGCAGGCCCGGTGAGGGAATCCCGAGGCTTAAGC 300
QY 301 CCGGTGCACTGATGCTTCAAGCCTGTGTCTGAGCAGCCAGCCCTACTGCTAGC 360
DB 301 CCGGTGCACTGATGCTTCAAGCCTGTGTCTGAGCAGCCAGCCCTACTGCTAGC 360
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DB 601 AGCTGAGGCCATGAGAGAGGGGCAAGTTCTCTCTGAGAGGTTATTCGTAAGCAGT 660
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DB 661 GGAACAGACAAAGGCCAGGGGAGCTAACCCGAGATCCAGCCCGGCTCACTCCGTTG 720
QY 721 GCTCAGGCAATATCTTAACCTCTCTGAGGCTCTCTGAGCCCTACAGGATCAAGT 780
DB 721 GCTCAGGCAATATCTTAACCTCTCTGAGGCTCTCTGAGCCCTACAGGATCAAGT 780
QY 781 AGGGGGGTGAGAGAACCCAGACAGTGAAGCCTTTTAACATTTCTCGGGGTGAGCAGC 840
DB 781 AGGGGGGTGAGAGAACCCAGACAGTGAAGCCTTTTAACATTTCTCGGGGTGAGCAGC 840
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DB 841 CCTTCCCAAAATGCTGTGTGCTGACAGCTGTGTGTGTGTAGGGGTCCCAACGGGCTC 900
QY 901 AGTGTGGGTGAGGCTGTGCTGAACTGGGACAGGGGTCTCAGAAAGGCTCTCTCCTC 960
DB 901 AGTGTGGGTGAGGCTGTGCTGAACTGGGACAGGGGTCTCAGAAAGGCTCTCTCCTC 960
QY 961 TGCCCACTGGGATAGGCTCTGAGGAGCTGGAGCATGTGATCTCACTGATGACCTGG 1020
DB 961 TGCCCACTGGGATAGGCTCTGAGGAGCTGGAGCATGTGATCTCACTGATGACCTGG 1020
QY 1021 CCTTTCGCCAGAGCCAGGCTCTCAACAGCTGAGAGCCCGGCTTAACAAGTTCAACTCA 1080
DB 1021 CCTTTCGCCAGAGCCAGGCTCTCAACAGCTGAGAGCCCGGCTTAACAAGTTCAACTCA 1080
QY 1081 TTGCTGAGGTGTGAGAAAGTCCGACAGCCGTGTCTCACTAAGAGCTCTTCTGAAC 1140
DB 1081 TTGCTGAGGTGTGAGAAAGTCCGACAGCCGTGTCTCACTAAGAGCTCTTCTGAAC 1140
QY 1141 ACCGCTGTTTGGCCGAGAGGCTCTGTCAAGGGTTCTGAGCTTCACTATGTGAGG 1200
DB 1141 ACCGCTGTTTGGCCGAGAGGCTCTGTCAAGGGTTCTGAGCTTCACTATGTGAGG 1200
QY 1201 CCGGCTTATATCAATCAAGTCCCAAGTGTCTGAGCAAGTGTCTGAGCAAGTGTCTG 1260
DB 1201 CCGGCTTATATCAATCAAGTCCCAAGTGTCTGAGCAAGTGTCTGAGCAAGTGTCTG 1260

Oy	2341	GTGAACCCCACTGCAAGTATCCCTCTCTCTGCCCTCTCTCACTGCAAGTCTGGGCTGCC	2400
Db	2341	GTGAACCCCACTGCAAGTATCCCTCTCTCTGCCCTCTCTCACTGCAAGTCTGGGCTGCC	2400
Oy	2401	AAGCTTCTTCCCTCCCTGACAAACGCCCACTGACCTGAGAGCCCAAGTCTCTCTGCCCT	2460
Db	2401	AAGCTTCTTCCCTCCCTGACAAACGCCCACTGACCTGAGAGCCCAAGTCTCTCTGCCCT	2460
Oy	2461	AGGACTTACCAAGCTGTAAGGGCCAGGGCTGTGTGCTTCCAGCTTGGGGTCCCTTGAGAGAC	2520
Db	2461	AGGACTTACCAAGCTGTAAGGGCCAGGGCTGTGTGCTTCCAGCTTGGGGTCCCTTGAGAGAC	2520
Oy	2521	AGGACACATCATGATCCCTTTGGGGGTGGGGGGGTGGGGTCCAGCCACAGACAGGACATGAG	2580
Db	2521	AGGACACATCATGATCCCTTTGGGGGTGGGGGGGTGGGGTCCAGCCACAGACAGGACATGAG	2580
Oy	2581	TGAAATGCCCTCTGCTGTGGAGCTGAGCCCGCCCTTGCATGAGATTTTCTCCCAAGCC	2640
Db	2581	TGAAATGCCCTCTGCTGTGGAGCTGAGCCCGCCCTTGCATGAGATTTTCTCCCAAGCC	2640
Oy	2641	AGGACAGAGGCGCGGGGGGAGACGCTGGAAGTTGGCTGTGCTGCGCGGGGAAGCTTCTCTC	2700
Db	2641	AGGACAGAGGCGCGGGGGGAGACGCTGGAAGTTGGCTGTGCTGCGCGGGGAAGCTTCTCTC	2700
Oy	2701	CCCAAGCGGCGCATGAGGAGCAAGCTGCAAGAGACAGTGAAGCTGCGGGGTGTGAG	2760
Db	2701	CCCAAGCGGCGCATGAGGAGCAAGCTGCAAGAGACAGTGAAGCTGCGGGGTGTGAG	2760
Oy	2761	GACTGAGCCGGCTTCCCTTCCCAAGAGCTGTGGGATGAGAGACCGGCTGTGATGAG	2820
Db	2761	GACTGAGCCGGCTTCCCTTCCCAAGAGCTGTGGGATGAGAGACCGGCTGTGATGAG	2820
Oy	2821	TGCCGCCAGAGGAGCATCAGGCTGTGCTGGGACCAACCCCTCATATCCAGGGAAGATGTGT	2880
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RESULT 3			
US-10-485-313A-31			
; Sequence 31, Application US/10485313A			
; Publication No. US2005005902A1			
; GENERAL INFORMATION:			
; APPLICANT: NIE, Guiying			
; APPLICANT: SALAMONSEN, Lois Adrienne			
; APPLICANT: LI, Ying			
; APPLICANT: HAMPTON, Anne Lorraine			
; APPLICANT: FINDLAY, John Kerr			
; TITLE OF INVENTION: Novel Serine Protease			
; FILE REFERENCE: 31633-200357			
; CURRENT APPLICATION NUMBER: US/10/485,313A			
; CURRENT FILING DATE: 2004-01-30			
; PRIOR APPLICATION NUMBER: PCT/AU02/01010			
; PRIOR FILING DATE: 2002-07-30			
; PRIOR APPLICATION NUMBER: PR6707			
; PRIOR FILING DATE: 2001-07-30			
; NUMBER OF SEQ ID NOS: 55			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 31			
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; TYPE: DNA			
; ORGANISM: Homo sapiens			

US-10-485-313A-31

Query Match	65.3%	Score 1962.2	DB 9	Length 2543
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1964	Conservative 0	Mismatches 3	Indels 0	Gaps 0
QY 1038	GGTCTCCACGACCTGAGCAGCCCGGCTCAAGTTCAATTGATGCTGACGCTGAG	1097		
DB 577	GGTCTCCACGACCTGAGCAGCCCGGCTCAAGTTCAATTGATGCTGACGCTGAG	636		
QY 1098	AAGATGCAACGACCGGTGCTCAATAGAGCTCTTCTGAGAACCCTGTTTGCCGC	1157		
DB 637	AAGATGCAACGACCGGTGCTCAATAGAGCTCTTCTGAGACCCCTGTTTGCCGC	696		
QY 1158	AACGTGCCCTTCCAGCGGTTCTGGCTTCAATGTCAGAGCCCGCTGATCATCAC	1217		
DB 697	AACGTGCCCTTCCAGCGGTTCTGGCTTCAATGTCAGAGCCCGCTGATCATCAC	756		
QY 1218	AATGCCACGTGTGTCAGCAACGTGCTGCCCGGAGGAGGAGGAGCTCAAGTGAG	1277		
DB 757	AATGCCACGTGTGTCAGCAACGTGCTGCCCGGAGGAGGAGGAGCTCAAGTGAG	816		
QY 1278	CTACAGAAATGGGAGCTCTATAGAGGCAATCAAGAATGAGATGAGCAT	1337		
DB 817	CTACAGAAATGGGAGCTCTATAGAGGCAATCAAGAATGAGATGAGCAT	876		
QY 1338	GCCACCATCAAGATCATCTCCAGAAAGATCTCCGTGTGTGTGTGTGTGTGTGT	1397		
DB 877	GCCACCATCAAGATCATCTCCAGAAAGATCTCCGTGTGTGTGTGTGTGTGTGT	936		
QY 1398	GACCTGCGGCTTGGGAGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1457		
DB 937	GACCTGCGGCTTGGGAGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	996		
QY 1458	GTAACAACGGGATCTGTCAGCACTGCCAGCGGAGGAGGAGGAGGAGGAGGAG	1517		
DB 997	GTAACAACGGGATCTGTCAGCACTGCCAGCGGAGGAGGAGGAGGAGGAGGAG	1056		
QY 1518	TCCGACATGAGATCATCTCAAGACGATGCTCATCATCACTACGGGAACTCCGGGGAG	1577		
DB 1057	TCCGACATGAGATCATCTCAAGACGATGCTCATCATCACTACGGGAACTCCGGGGAG	1116		
QY 1578	CTGGTGAACCTGAGATGAGGAGGATTTGGATCAACAGCTCAAGGTTCAAGGCTGAG	1637		
DB 1117	CTGGTGAACCTGAGATGAGGAGGATTTGGATCAACAGCTCAAGGTTCAAGGCTGAG	1176		
QY 1638	TCCCTTGGCATCCCTCAGACCGCATCACACGCTTCTTCAAGAGTTCCAGACAGCAG	1697		
DB 1177	TCCCTTGGCATCCCTCAGACCGCATCACACGCTTCTTCAAGAGTTCCAGACAGCAG	1236		
QY 1698	ATCAAGATGAGAAAGGCTTTCATGCGATACGATGCGGACGATCAACAGCCTG	1757		
DB 1237	ATCAAGATGAGAAAGGCTTTCATGCGATACGATGCGGACGATCAACAGCCTG	1296		
QY 1758	GTAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1817		
DB 1297	GTAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1356		
QY 1818	CAAGAGGTTGCGCGCAATTCACCTTCTCAGAGAGGCGGATCAAGATGATCATCATC	1877		
DB 1357	CAAGAGGTTGCGCGCAATTCACCTTCTCAGAGAGGCGGATCAAGATGATCATCATC	1416		
QY 1878	GTAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1937		
DB 1417	GTAAGTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1476		
QY 1938	GAGTCTCCCT	1997		
DB 1477	GAGTCTCCCT	1536		
QY 1998	CCTGAAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2057		
DB 1537	CCTGAAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	1596		

QY 2058	ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2117		
DB 1597	ACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1656		
QY 2118	GACAGCT	2177		
DB 1657	GACAGCT	1716		
QY 2178	TTTCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2237		
DB 1717	TTTCCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1776		
QY 2238	CTTGTACAGATGATCTGAAAGTCACTTCAAGTTCTCCGATATTCACAAACGCTT	2297		
DB 1777	CTTGTACAGATGATCTGAAAGTCACTTCAAGTTCTCCGATATTCACAAACGCTT	1836		
QY 2298	CCATGAGGATCCCT	2357		
DB 1837	CCATGAGGATCCCT	1896		
QY 2358	GATCCCTGCTCTGCT	2417		
DB 1897	GATCCCTGCTCTGCT	1956		
QY 2418	ACAAACGCGCACTGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2477		
DB 1957	ACAAACGCGCACTGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2016		
QY 2478	AGGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2537		
DB 2017	AGGAGCAGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2076		
QY 2538	TTTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2597		
DB 2077	TTTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2136		
QY 2598	CGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2657		
DB 2137	CGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2196		
QY 2658	GAGCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2717		
DB 2197	GAGCAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2256		
QY 2718	GAGCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2777		
DB 2257	GAGCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2316		
QY 2778	CTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2837		
DB 2317	CTTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2376		
QY 2838	CAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2897		
DB 2377	CAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2436		
QY 2958	AAATTAAGTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	3004		
DB 2497	AAATTAAGTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	2543		

RESULT 4
US-10-956-157-5181
; Sequence 5181, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William

! TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
! FILE REFERENCE: 031896-043000 (AM 101081)
! CURRENT APPLICATION NUMBER: US/10/956,157
! NUMBER OF SEQ ID NOS: 319805
! SOFTWARE: Patent version 3.2
! SEQ ID NO 5181
! LENGTH: 2541
! TYPE: DNA
! ORGANISM: Homo sapiens
US-10-956-157-5181

Query Match 65.0%; Score 1953; DB 9; Length 2541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1953; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 GGTCTCCACCAAGCTGAGCAGCCCGCTACAGATTCAATTGCTGACGTGTGAG 1097
DB GGTCTCCACCAAGCTGAGCAGCCCGCTACAGATTCAATTGCTGACGTGTGAG 648
QY 1098 AATATGACACCAAGCTGTGCTCATTAGACTCTTCTGAGACCCGCTGTTGGCCG 1157
DB AATATGACACCAAGCTGTGCTCATTAGACTCTTCTGAGACCCGCTGTTGGCCG 708
QY 1158 AACGTGCCCCCTGTCAGACGGGTTCTGCTTCAATGATGACAGGCGGAGCTGATCATACC 1217
DB AACGTGCCCCCTGTCAGACGGGTTCTGCTTCAATGATGACAGGCGGAGCTGATCATACC 768
QY 1218 AATGCCACGTGTGTCTCAGCAACAGTCTGCCCCGGGACGAGCAGCTCAAGGTGAG 1277
DB AATGCCACGTGTGTCTCAGCAACAGTCTGCCCCGGGACGAGCAGCTCAAGGTGAG 828
QY 1278 CTACAAATGGGGACCTCTTATGAGGCACTCAATGAATGCAAGAAGTGGACATT 1337
DB CTACAAATGGGGACCTCTTATGAGGCACTCAATGAATGCAAGAAGTGGACATT 888
QY 1338 GCCACATCAAGTCCATCCCAAGAAAAGCTCCCTGTGTTGCTGGGTCATCTGGCC 1397
DB GCCACATCAAGTCCATCCCAAGAAAAGCTCCCTGTGTTGCTGGGTCATCTGGCC 948
QY 1398 GACCTGCGGCTGGGAGATTGTGTGGCCATCGGAGTCCCTTGGCCCTACAGAACACA 1457
DB GACCTGCGGCTGGGAGATTGTGTGGCCATCGGAGTCCCTTGGCCCTACAGAACACA 949
QY 1458 GTGACAAAGGGGATCTCTCAGCACTGCCAGCGGAGGAGGAGGCTGCGGAGC 1517
DB GTGACAAAGGGGATCTCTCAGCACTGCCAGCGGAGGAGGAGGCTGCGGAGC 1068
QY 1518 TCCGATGGAATCACTACAGACGATGATCATCACTACGGAATCCGCGGAGCA 1577
DB TCCGATGGAATCACTACAGACGATGATCATCACTACGGAATCCGCGGAGCA 1128
QY 1578 CTGGTGAACCTGATGAGCAGAGTCACTTGGATCAACAGCTCAAGGTCACGGCTGGATC 1637
DB CTGGTGAACCTGATGAGCAGAGTCACTTGGATCAACAGCTCAAGGTCACGGCTGGATC 1129
QY 1638 TCTTTGGCATCCCTCAGACCGCATCACAGGTTTCTCAGAGTTTCCAAGACAGCAG 1697
DB TCTTTGGCATCCCTCAGACCGCATCACAGGTTTCTCAGAGTTTCCAAGACAGCAG 1189
QY 1698 ATCAAGAAGCTGAAAGAGCTTCACTGAGCATAGAGTGGAGCATCAACAGACCTG 1757
DB ATCAAGAAGCTGAAAGAGCTTCACTGAGCATAGAGTGGAGCATCAACAGACCTG 1249
QY 1758 GTGGATGAGCTGAAGGCGCAACCCGGAATTCCAGAGTCAAGAGTGAATTTATGTC 1817
DB GTGGATGAGCTGAAGGCGCAACCCGGAATTCCAGAGTCAAGAGTGAATTTATGTC 1309
QY 1818 CAAGAGTTGGCGCGAATTCATCTTCAAGAGGCGGATCCAGAGTGTGATCATC 1877
DB CAAGAGTTGGCGCGAATTCATCTTCAAGAGGCGGATCCAGAGTGTGATCATC 1368
QY 1877 CAAGAGTTGGCGCGAATTCATCTTCAAGAGGCGGATCCAGAGTGTGATCATC 1428

QY 1878 GTCAAGTCAACGGGCGTCTCTAGTAGACTGAGTAGCTGACAGAGCGGTGAC 1937
DB GTCAAGTCAACGGGCGTCTCTAGTAGACTGAGTAGCTGACAGAGCGGTGAC 1429
QY 1938 GAGTCTCTCTCTACTGAGGTGCGGCGGAAAGAGACCTTCTTTCAGATCGCA 1997
DB GAGTCTCTCTCTACTGAGGTGCGGCGGAAAGAGACCTTCTTTCAGATCGCA 1489
QY 1998 CTTGAGGTGTATGTGAGGGGCGATTTCTTACAGCCGACAGCTTCAAGCTGAGACA 2057
DB CTTGAGGTGTATGTGAGGGGCGATTTCTTACAGCCGACAGCTTCAAGCTGAGACA 1549
QY 2058 ACGAGGGGAGCGCCCGCCGATCAGAGCAAGAGCAACCGTGTCTTCAAGAGGAC 2117
DB ACGAGGGGAGCGCCCGCCGATCAGAGCAAGAGCAACCGTGTCTTCAAGAGGAC 1609
QY 2118 GGGACCTTCTCTGTGCTGTCCGGGAGAGCGAGGCTTGTGACCAAGGCGCGAA 2177
DB GGGACCTTCTCTGTGCTGTCCGGGAGAGCGAGGCTTGTGACCAAGGCGCGAA 1669
QY 2178 TTTCCGCTGGGAGATGTTGATCCCATCCCGGTGCGGGAGGAGGCCCAATGCC 2237
DB TTTCCGCTGGGAGATGTTGATCCCATCCCGGTGCGGGAGGAGGCCCAATGCC 1729
QY 2238 CTGTACAGATGATCTGAAAGTCACTTCAAGTTCTCCGATATTCAAAATGACCTT 2297
DB CTGTACAGATGATCTGAAAGTCACTTCAAGTTCTCCGATATTCAAAATGACCTT 1789
QY 2298 CCATGAGGTGCTCTCTCTCTAGCTTCCGCTCTGAGGAGCAACCATCTGCA 2357
DB CCATGAGGTGCTCTCTCTCTAGCTTCCGCTCTGAGGAGCAACCATCTGCA 1849
QY 2358 GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2417
DB GATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1909
QY 2418 ACAAAGCCCACTGACCTGAGGCCCAAGCTTCCCTGCTGAGCTTACCAAGCTGT 2477
DB ACAAAGCCCACTGACCTGAGGCCCAAGCTTCCCTGCTGAGCTTACCAAGCTGT 1969
QY 2478 AGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2537
DB AGGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2029
QY 2538 TTTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 2597
DB TTTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 2089
QY 2598 CGAGCTGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2657
DB CGAGCTGAGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2149
QY 2658 GAGCAGTGAAGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2717
DB GAGCAGTGAAGTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2209
QY 2718 GCAAGCTGAGAGCACTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2777
DB GCAAGCTGAGAGCACTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2269
QY 2778 CTTCCAGCAGCTTGTGGATGACAGACCGCTGCAATGAAAGTGCAGGAGGATG 2837
DB CTTCCAGCAGCTTGTGGATGACAGACCGCTGCAATGAAAGTGCAGGAGGATG 2339
QY 2838 CAGGCTGCTGAGCAACCCCTCATCAAGGAAAGAGTGTCTCAAGGAGGCAATTTGTG 2897
DB CAGGCTGCTGAGCAACCCCTCATCAAGGAAAGAGTGTCTCAAGGAGGCAATTTGTG 2389
QY 2898 AGCTTTGTGTAATGAAATTCAGAGTGTGCTTCACTGATGATGTTCTCTAATGAG 2957
DB AGCTTTGTGTAATGAAATTCAGAGTGTGCTTCACTGATGATGTTCTCTAATGAG 2449
QY 2958 AAATTAAGTTTACAGACAGGTTCTCAGCA 2990

[illegible]

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Db      2526 AACTAAAGTTTACAGACACAAAAAAAAAAAAAAAAAAAAAA 2567

RESULT 7
US-09-764-898-112
; Sequence 112, Application US/09764898
; Patent No. US2002090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: Puz01
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 112
; LENGTH: 1868
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-898-112

Query Match          60.3%; Score 1813.8; DB 3; Length 1868;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 1818; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY      1174 GGGGTTCTGGGCTTCATCATGTCCAGAGCGCGGCTGCATCATCAACCAATGCCACGNGTG 1233
DB      21 GGGGTTCTGGCTTCATCATGTCCAGAGCGCGGCTGCATCATCAACCAATGCCACGNGTG 80

QY      1234 CCAGCAACAGTGTCTGCCCCCGGAGCAGCAGCTCAAGTGCAGCTACAGAATGGGA 1293
DB      81 CCAGCAACAGTGTCTGCCCCCGGAGCAGCAGCTCAAGTGCAGSTACAGAATGGGA 140

QY      1294 CCTATGAGGCCCATCAAAGCATCGACAGAAAGTCCGAATTGCCCATCAAGATCC 1355
DB      141 CCTATGAGGCCCATCAAAGCATCGACAGAAAGTCCGAATTGCCCATCAAGATCC 200

QY      1354 ATCCCAAAAAGAGTCCCTGTTGTTGTTCAGGAGTCACTCGGCGCACTCGGCGCTTG 1411
DB      201 ATCCCAAAAAGAGTCCCTGTTGTTGTTCAGGAGTCACTCGGCGCACTCGGCGCTTG 260

QY      1414 AGTTTGTGTGGCCCATTCGCGAGTCCCTTGCCTTACAGAACACAGTCAACCGGCATCG 1473
DB      261 AGTTTGTGTGGCCCATTCGCGAGTCCCTTGCCTTACAGAACACAGTCAACCGGCATCG 320

QY      1474 TCAGCACTGCCOAGCGGAGGCGAGGAGTGGGCTTCGGGACTTCGACATGACATA 1533
DB      321 TCAGCACTGCCOAGCGGAGGCGAGGAGTGGGCTTCGGGACTTCGACATGACATA 380

QY      1534 TTCCAACGGAATGCCATCATCAATCAACGGAATCTCCGGGGACA CACTGGTGAACCTGAGTG 1599
DB      381 TTCCAACGGAATGCCATCATCAATCAACGGAATCTCCGGGGACA CACTGGTGAACCTGAGTG 440

QY      1594 GCGAGGTGATTGGGATCAACACGCTCAAGGTTCACGCGTGGCATCTCTTGGCATCCCT 1653
DB      441 GCGAGGTGATTGGGATCAACACGCTCAAGGTTCACGCGTGGCATCTCTTGGCATCCCT 500

QY      1654 CAGACCGCATCACACGTTCTCTCAACAGTTCCAGATCCAGACAGATCAAAGATGGAAGA 1713
DB      501 CAGACCGCATCACACGTTCTCTCAACAGTTCCAGATCCAGACAGATCAAAGATGGAAGA 560

QY      1714 AGCGTTTATGGGATACGATGGGAGTGCAGATCAACCAAGCTGTGTGATGAGCTGAAG 1773
DB      561 AGCGTTTATGGGATACGATGGGAGTGCAGATCAACCAAGCTGTGTGATGAGCTGAAG 620

QY      1774 CCAGCAACCCGGAATCTCCCAAGGTTCAGACATGGAATTTATGTCCAAAGGTTGCGCGA 1833
DB      621 CCAGCAACCCGGAATCTCCCAAGGTTCAGACATGGAATTTATGTCCAAAGGTTGCGCGA 680

QY      1834 ATTCACTTTCAAGAGGCGGCATCCCAAGTGGTGAATCATATGTCAAAGTCAA CGGCG 1893

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Db 681 ATTCACTTCTCAGAGAGCGGCATCCAAAGATGTGACATATCGTCAAAGTCAAGGCG 740
QY 1894 GTTCCTAGTAGACTGAGTAGCTGACAGAGAGCGGTGTGACCGAGTCTCTCTCTAC 1953
Db 741 GTCTCTAGTAGACTGAGTAGCTGACAGAGAGCGGTGTGACCGAGTCTCTCTCTAC 800
QY 1954 TGGAGGTGGCGCGGGGAAAGACAGACCTCTCTTACGATCGCACTTGAAGTGTGTATCT 2013
Db 801 TGGAGGTGGCGCGGGGAAAGACAGACCTCTCTTACGATCGCACTTGAAGTGTGTATCT 860
QY 2014 GAGGGGCGGATCTCTCAGCGGCAAGCGCTCAGAGCGCTGAGCAAAAGAGGCGAGCGCC 2073
Db 861 GAGGGGCGGATCTCTCAGCGGCAAGCGCTCAGAGCGCTGAGCAAAAGAGGCGAGCGCC 920
QY 2074 CCCCAGATCAGAGACGAGAGCAACCGTGTCTTACAGAGGGCGGACGCTCTCTGG 2133
Db 921 CCCCAGATCAGAGACGAGAGCAACCGTGTCTTACAGAGGGCGGACGCTCTCTGG 980
QY 2134 CTGTCCGGGGCAGAGCGAGGCTGGGCTTGGCCAGGGGCGGCAATTTCCGCTGGGGAGT 2193
Db 981 CTGTCCGGGGCAGAGCGAGGCTGGGCTTGGCCAGGGGCGGCAATTTCCGCTGGGGAGT 1040
QY 2194 GTTGAATCAATCCCGGTGGCGGGAGGAGCCCAATCCCTTGTATAGATGATCC 2253
Db 1041 GTTGAATCAATCCCGGTGGCGGGAGGAGCCCAATCCCTTGTATAGATGATCC 1100
QY 2254 TGAAGTCACTTCAAGTTCTCCGATATTCAAAATGCTCTTCAATGAGTCCCTTC 2313
Db 1101 TGAAGTCACTTCAAGTTCTCCGATATTCAAAATGCTCTTCAATGAGTCCCTTC 1160
QY 2314 CTCTCTAGCTTCCCGCTCTGCGGCTTGGAGAACCATCTGCAAGTATCCCTGCTCTG 2373
Db 1161 CTCTCTAGCTTCCCGCTCTGCGGCTTGGAGAACCATCTGCAAGTATCCCTGCTCTG 1220
QY 2374 CCCCTCTACTGAGGTCTGGGCTGGCAAGCTTCTTCCCGCTGACAAAGCCCACTGA 2433
Db 1221 CCCCTCTACTGAGGTCTGGGCTGGCAAGCTTCTTCCCGCTGACAAAGCCCACTGA 1280
QY 2434 CTTGAGGCGCCAGCTTCTCTGCGCTTGAAGATTTACCAAGCTTGAAGGCGAGGCTGCG 2493
Db 1281 CTTGAGGCGCCAGCTTCTCTGCGCTTGAAGATTTACCAAGCTTGAAGGCGAGGCTGCG 1340
QY 2494 CTTGAGGCGCTGGGGTCTCTGAGAGACAGGTCACTGTATCTTGGGGTCTGGGGGT 2553
Db 1341 CTTGAGGCGCTGGGGTCTCTGAGAGACAGGTCACTGTATCTTGGGGTCTGGGGGT 1400
QY 2554 GGGGTCAAGCCCAAGAGGCACTGAGTAATGCCCCCTGGCTGGAGGCTGAGCCCGC 2613
Db 1401 GGGGTCAAGCCCAAGAGGCACTGAGTAATGCCCCCTGGCTGGAGGCTGAGCCCGC 1460
QY 2614 CTTGCAATGATTTTCTCTCCCAAGGCAAGGCGCGGGGAGCAAGTGAAGTT 2673
Db 1461 CTTGCAATGATTTTCTCTCCCAAGGCAAGGCGCGGGGAGCAAGTGAAGTT 1520
QY 2674 GGTGCTGCTGGGGAGTCTTCTCTCCCAAGGCGGCAATGGGGCAAGCTGAGAGAC 2733
Db 1521 GGTGCTGCTGGGGAGTCTTCTCTCCCAAGGCGGCAATGGGGCAAGCTGAGAGAC 1580
QY 2734 AGTGAAGTGAAGCTGGGGGTGTGAGACTGAGCCCGCTTCCCAAGGAGCTCT 2793
Db 1581 AGTGAAGTGAAGCTGGGGGTGTGAGACTGAGCCCGCTTCCCAAGGAGCTCT 1640
QY 2794 GGGATGAGAGAGCGCTCGATGGAAGTGCGCGCCAGAGGAGATCAGGCTGTGGGAGC 2853
Db 1641 GGGATGAGAGAGCGCTCGATGGAAGTGCGCGCCAGAGGAGATCAGGCTGTGGGAGC 1700
QY 2854 ACCGCTCATTCAGAGGAGAGAGTGTCTCAAGGGGCAATTTGAGGCTTGTCTGAATG 2913
Db 1701 ACCGCTCATTCAGAGGAGAGAGTGTCTCAAGGGGCAATTTGAGGCTTGTCTGAATG 1760
QY 2914 GATTCCAGTGTCTGTATCTGTATTTTCTCACTGTATGAAATTAAGTTTAAG 2973
Db 1761 GATTCCAGTGTCTGTATCTGTATTTTCTCACTGTATGAAATTAAGTTTAAG 1820

QY 2974 CACAGCTTCTCAGCGCAAAAAAAAAAAAAAAAA 3006
Db 1821 CACAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1853
RESULT 8
US-10-301-822-78
; Sequence 78, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TREATMENT OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RUM
; CURRENT APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 2551
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (222)...(1580)
US-10-301-822-78
Query Match 59.3%; Score 1783; DB 6; Length 2551;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1928; Conservative 0; Mismatches 15; Indels 16; Gaps 12;
QY 1038 GGTCTCCACAGCTGAGCGCCGCGCTCAAGTTCATCTTACGTGAGTGTGAG 1097
Db 606 GGTCTCCACAGCTGAGCGCCGCGCTCAAGTTCATCTTACGTGAGTGTGAG 665
QY 1098 AAGATGCAACAGCCGCTGTGCAATGAGCTTCTCTGAGACACCCGCTGTTGGCCGC 1157
Db 666 AAGATGCAACAGCCGCTGTGCAATGAGCTTCTCTGAGACACCCGCTGTTGGCCGC 725
QY 1158 AACGTGCCCTGTCCAGCGGTTCTGGCTTCAATCATCTCAGAGCGCGGATCATCAC 1217
Db 726 AACGTGCCCTGTCCAGCGGTTCTGGCTTCAATCATCTCAGAGCGCGGATCATCAC 785
QY 1218 AATGCCAAGTGTGTCAGAACAGTGTGCTGCCCGGAGGAGGAGCTCAAGGTGAG 1277
Db 786 AATGCCAAGTGTGTCAGAACAGTGTGCTGCCCGGAGGAGGAGCTCAAGGTGAG 845
QY 1278 CTACAGAAATGGGAGCTCTATGAGGCGCACCATCAAGACATGACAAAGTCTGAGCAT 1337
Db 846 CTACAGAAATGGGAGCTCTATGAGGCGCACCATCAAGACATGACAAAGTCTGAGCAT 905
QY 1338 GCCACATCAAGATTCATCCCAAGAAAGCTCCGTGTGTGTGCTGGGCTCACTGGCC 1397
Db 906 GCCACATCAAGATTCATCCCAAGAAAGCTCCGTGTGTGTGCTGGGCTCACTGGCC 965
QY 1398 GACCTGCGCTGGGAGTGTGTGTGTCATCGGAGTCCCTTCCGCTTACAGAACACA 1457
Db 966 GACCTGCGCTGGGAGTGTGTGTGTCATCGGAGTCCCTTCCGCTTACAGAACACA 1023


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Db      421  TGTGAGGGGGCGGCGATTCCTCCAGCGCCAGCGTCAGAGCCTGACGACAAAGAGGGGCGAGG 480
Qy      2071  CCCCCCGAGATCAGAGAGAGAGACCAAGTGGTCTTCAGAGAGGGGCGGCGACCTCTCC 2130
Db      481  CCCCCCGAGATCAGAGAGAGAGACCAAGTGGTCTTCAGAGAGGGGCGGCGACCTCTCC 540
Qy      2131  TGGCTGTCGGGGGCGAGAGCGAGGCTGGGCTTGGCCAGGGGCGGCAATTTCCGCTGGG 2190
Db      541  TGGCTGTCGGGGGCGAGAGCGAGGCTGGGCTTGGCCAGGGGCGGCAATTTCCGCTGGG 600
Qy      2191  AGTGTGATTCACATCCCGGTGCGGGAGGAGGAGCCCAACATCCCTTTGACAGATGA 2250
Db      601  AGTGTGATTCACATCCCGGTGCGGGAGGAGGAGCCCAACATCCCTTTGACAGATGA 660
Qy      2251  TCCCTAAGTCACTTCCAAAGTTCTCCGATATTCACAAACCTGCTTCAATGAGATGCC 2310
Db      661  TCCCTAAGTCACTTCCAAAGTTCTCCGATATTCACAAACCTGCTTCAATGAGATGCC 720
Qy      2311  CTCCTCTCTAGCTTCCGCGCTCTGCGCCCTGTGAAACACCATCTGAGATATCCCTGCTC 2370
Db      721  CTCCTCTCTAGCTTCCGCGCTCTGCGCCCTGTGAAACACCATCTGAGATATCCCTGCTC 780
Qy      2371  CTGCCCCCTCTCACTGCAAGGCTCTGCGCCCTGTGAAACACCATCTGAGATATCCCTGCTC 2430
Db      781  CTGCCCCCTCTCACTGCAAGGCTCTGCGCCCTGTGAAACACCATCTGAGATATCCCTGCTC 840
Qy      2431  TGACCTGAGAGCCCGGAGCTTCCCTCTGCGCCCTGTGAAACACCATCTGAGATATCCCTGCTC 2490
Db      841  TGACCTGAGAGCCCGGAGCTTCCCTCTGCGCCCTGTGAAACACCATCTGAGATATCCCTGCTC 900
Qy      2491  CTGCGTCGACGCTTGGGGGTCCTGTGAGAGACAGTCAATCTGATCCCTTTGGGGTGGGG 2550
Db      901  CTGCGTCGACGCTTGGGGGTCCTGTGAGAGACAGTCAATCTGATCCCTTTGGGGTGGGG 960
Qy      2551  GGTGGGGGTTCAGAGCCCGAGAGAGCACTGAGTAAATGCCCCCTGAGCTGCGAGCTGAGCCC 2610
Db      961  GGTGGGGGTTCAGAGCCCGAGAGAGCACTGAGTAAATGCCCCCTGAGCTGCGAGCTGAGCCC 1020
Qy      2611  CGCCCTGCGATGAGGTTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2670
Db      1021  CGCCCTGCGATGAGGTTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy      2671  GTTGGCTGCTGCTTGGGGAGAGTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2730
Db      1081  GTTGGCTGCTGCTTGGGGAGAGTTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
Qy      2731  GACAGTGAAGCTGAGAGCTGCGGGGTGTGAGAGACTGAGCGGCTTCCCTTCCAGAGAGAG 2790
Db      1141  GACAGTGAAGCTGAGAGCTGCGGGGTGTGAGAGACTGAGCGGCTTCCCTTCCAGAGAGAG 1200
Qy      2791  TCTGGAGATGACAGAGCCGCTGCGATGAAAGTCCCGCCAGAGAGAGAGAGAGAGAGAGAG 2850
Db      1201  TCTGGAGATGACAGAGCCGCTGCGATGAAAGTCCCGCCAGAGAGAGAGAGAGAGAGAGAG 1260
Qy      2851  ACCAAGCCCTCTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2910
Db      1261  ACCAAGCCCTCTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
Qy      2911  ATGAGTCCAGAGTGTGCTTGTACTGTATGTTTCTCTACTGTATGAAATTAAGTTTAC 2970
Db      1321  ATGAGTCCAGAGTGTGCTTGTACTGTATGTTTCTCTACTGTATGAAATTAAGTTTAC 1380
Qy      2971  AAGCACAGGTTCTGAGCCA 2990
Db      1381  AAGCACAGGTTCTGAGCCA 1400

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RESULT 11
 US-10-275-505-28
 ; Sequence 28, Application US/10275505
 ; Publication No. US2004081961A1
 ; GENERAL INFORMATION:

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; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G.
; APPLICANT: HAPALIA, April J.A.; PATTERSON, Chandra
; APPLICANT: WALIA, Narinder K.; KEARNEY, Liam
; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda; ELIOTT, Vicki S.
; APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.
; APPLICANT: YANG, Junning; HERNANDEZ, Roberto
; APPLICANT: POLICKY, Jennifer L.; LU, Dyoung Ahna M.
; APPLICANT: REDDY, Koopa M.; YUE, Henry
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0085 USN
; CURRENT APPLICATION NUMBER: US/10/275,505
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/US01/14651
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/209,402
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/207,477
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/205,803
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/203,566
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/202,082
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474343CB1
US-10-275-505-28

Query Match      41.0%; Score 1233; DB 7; Length 1797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1098  GGTCTCCACGAGCTGAGAGAGCCGCGCTACAAAGTTCAACTTCAATGCTGAGTGGAG 1097
Db      555  GGTCTCCACGAGCTGAGAGAGCCGCGCTACAAAGTTCAACTTCAATGCTGAGTGGAG 624
Qy      1098  AAGATCGACAGCCGCTGCTCACTAGAGCTTCTCTGAGACACCGCTGTTTGGCGC 1157
Db      625  AAGATCGACAGCCGCTGCTCACTAGAGCTTCTCTGAGACACCGCTGTTTGGCGC 684
Qy      1158  AAGTGGCCCTGTCTCAAGGGTCTTGCCTTCAATCATGTCAAGAGCCGCGCTGATCAACC 1217
Db      685  AAGTGGCCCTGTCTCAAGGGTCTTGCCTTCAATCATGTCAAGAGCCGCGCTGATCAACC 744
Qy      1218  AATGCCAGGTGTCTCCAGAAAGTGTCTGCCCCGGGCAAGCACTCAAGTTGAG 1277
Db      745  AATGCCAGGTGTCTCCAGAAAGTGTCTGCCCCGGGCAAGCACTCAAGTTGAG 804
Qy      1278  CTACAGATGGGGAATCTCTATAGAGGCAACATCAAAAGCATTCGACAAAGTGGACATT 1337
Db      805  CTACAGATGGGGAATCTCTATAGAGGCAACATCAAAAGCATTCGACAAAGTGGACATT 864
Qy      1338  GCCACCATCAAGATCCATCCAAAGAAAGTCCCTGTGTTGTTGCTGGGTCACTCGGCC 1397
Db      865  GCCACCATCAAGATCCATCCAAAGAAAGTCCCTGTGTTGTTGCTGGGTCACTCGGCC 924
Qy      1398  GACCTGGGCTTGGGGAATTTGTGTGGCAATCGGCAATTCCTTCCGCTTCAAGAACCA 1457
Db      925  GACCTGGGCTTGGGGAATTTGTGTGGCAATCGGCAATTCCTTCCGCTTCAAGAACCA 984
Qy      1458  GTACACAGGAGCATGTGAGCACTGCGAGGGAGGAGGAGGAGCTGGGCTCCGGGAGC 1517

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Db 985 GTGACAAAGGAGCTGTGACGACCTGCGCAGGAGGAGGAGGAGCTGGGCTCCGGGAGC 1044
Qy 1518 TCCGACATGAGACTACATCCAGACGAGTGGCATATGATCAATCAAGGGAATCCGGGGAGCA 1577
Db 1045 TCCGACATGAGACTACATCCAGACGAGTGGCATATGATCAATCAAGGGAATCCGGGGAGCA 1104
Qy 1578 CTGGGAACTGGATGGGAGGCTGATGGCATCAACACGCTCAAGGCTGAGCTGGCATC 1637
Db 1105 CTGGGAACTGGATGGGAGGCTGATGGCATCAACACGCTCAAGGCTGAGCTGGCATC 1164
Qy 1638 TCCCTTGGCATCCCTCCAGACCGGATCAACGCTTCTTCAAGAGTTTCAAGACAGCAG 1697
Db 1165 TCCCTTGGCATCCCTCCAGACCGGATCAACGCTTCTTCAAGAGTTTCAAGACAGCAG 1224
Qy 1698 ATCAAGAGCTGGAAAGAGGCTTCAATCGGCAATACGATCGGAGCATCAACAGCCAG 1757
Db 1225 ATCAAGAGCTGGAAAGAGGCTTCAATCGGCAATACGATCGGAGCATCAACAGCCAG 1284
Qy 1758 GTGATGAGCTGAAAGGCGCAACCCGAGCTTCCAGAGGTCAGAGTGAATTTATGTG 1817
Db 1285 GTGATGAGCTGAAAGGCGCAACCCGAGCTTCCAGAGGTCAGAGTGAATTTATGTG 1344
Qy 1818 CAAGAGTTGGCCGCAATTCCTTCTCAAGAGGCGGCGCATCAAGATGCTGATCATC 1877
Db 1345 CAAGAGTTGGCCGCAATTCCTTCTCAAGAGGCGGCGCATCAAGATGCTGATCATC 1404
Qy 1878 GTCAAGGTCAGAGGAGGCTCTCTAGTGAAGCTGAGTGAAGGCTGAGGAGGCTGAGC 1937
Db 1405 GTCAAGGTCAGAGGAGGCTCTCTAGTGAAGCTGAGTGAAGGCTGAGGAGGCTGAGC 1464
Qy 1938 GAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1997
Db 1465 GAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1524
Qy 1998 CCTGAGTGTGATGAGAGGCGGCGCATCTCTCCAGGCGCAAGGCTGAGAGCTGAGAG 2057
Db 1525 CCTGAGTGTGATGAGAGGCGGCGCATCTCTCCAGGCGCAAGGCTGAGAGCTGAGAG 1584
Qy 2058 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2117
Db 1585 AGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1644
Qy 2118 GGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2177
Db 1645 GGCAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1704
Qy 2178 TTTCCGCTGGGAGAGTTGGATTCACATCCGCTGCGGAGGAGGAGGAGGAGGAGGAGG 2237
Db 1705 TTTCCGCTGGGAGAGTTGGATTCACATCCGCTGCGGAGGAGGAGGAGGAGGAGGAGG 1764
Qy 2238 CTTGTACAGATGATCTCTGAAGTCACTTCCAG 2270
Db 1765 CTTGTACAGATGATCTCTGAAGTCACTTCCAG 1797

RESULT 12
US-11-140-224-28
; Sequence 28, Application US/11140224
; Publication No. US20050227280A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELESEANE, Angelo M.; LATI, Preeti G.
; APPLICANT: HAPALITA, April J.; PATTERSON, Chandra
; APPLICANT: WALTA, Narinder K.; KEARNEY, Liam
; APPLICANT: TRIBOULET, Catherine M.; KHAN, Farrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
; APPLICANT: NGUYEN, Damiel B.; GANDHI, Ameena R.
; APPLICANT: YANG, Junming; HERNANDEZ, Roberto
; APPLICANT: POLICKY, Jennifer L.; LU, Dyrung Alina M.
; APPLICANT: REDDY, Koopa M.; YUE, Henry
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: PROTEASES
```

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; FILE REFERENCE: PI-0085 USN
; CURRENT APPLICATION NUMBER: US/11/140,224
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/10/275,505
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/US01/14651
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/209,402
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/207,477
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/205,803
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/203,566
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/202,082
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 7474343CB1
US-11-140-224-28

Query Match 41.0%; Score 1233; DB 10; Length 1797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1038 GGTCTCCACAGCTAGACAGCCCGGCTCAAAAGTTCAATTCATGTGACGTGGTGG 1097
Db 565 GGTCTCCACAGCTAGACAGCCCGGCTCAAAAGTTCAATTCATGTGACGTGGTGG 624
Qy 1098 AAGATCGACACAGCCGCTGCTCAATAGAGCTTTCTGAGACACCCGCTGTTGGCGGC 1157
Db 625 AAGATCGACACAGCCGCTGCTCAATAGAGCTTTCTGAGACACCCGCTGTTGGCGGC 684
Qy 1158 AACGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1217
Db 685 AACGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 744
Qy 1218 AATGCCAGTGTGTTCAGCAACAGTCTGCGGCGAGGAGGAGGAGGAGGAGGAGGAGG 1277
Db 745 AATGCCAGTGTGTTCAGCAACAGTCTGCGGCGAGGAGGAGGAGGAGGAGGAGGAGG 804
Qy 1278 CTACAGAAATGGGAACTCTATGAGGCGACCATCAAAAGCATGACAGAAAGTCGACATT 1337
Db 805 CTACAGAAATGGGAACTCTATGAGGCGACCATCAAAAGCATGACAGAAAGTCGACATT 864
Qy 1338 GCCACATCAAGATCCATCCCAAGAAAGCTCCCTGTTGTGTCCTGGGTCACTCGGCC 1397
Db 865 GCCACATCAAGATCCATCCCAAGAAAGCTCCCTGTTGTGTCCTGGGTCACTCGGCC 924
Qy 1398 GACCTGGGCTGGGGAAGTTTGTGTGGCATCGGAGTCCCTTGGCCTTACAGAACCA 1457
Db 925 GACCTGGGCTGGGGAAGTTTGTGTGGCATCGGAGTCCCTTGGCCTTACAGAACCA 984
Qy 1458 GTGACAAAGGAGCTGTGACGACCTGCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1517
Db 985 GTGACAAAGGAGCTGTGACGACCTGCCAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 1044
Qy 1518 TCCGACATGAGACTACATCCAGACGAGTGGCATATGATCAATCAAGGGAATCCGGGGAGCA 1577
Db 1045 TCCGACATGAGACTACATCCAGACGAGTGGCATATGATCAATCAAGGGAATCCGGGGAGCA 1104
Qy 1578 CTGGGAACTGGATGGGAGGCTGATGGCATCAACACGCTCAAGGCTGAGCTGGCATC 1637
Db 1105 CTGGGAACTGGATGGGAGGCTGATGGCATCAACACGCTCAAGGCTGAGCTGGCATC 1164
Qy 1638 TCCCTTGGCATCCCTCCAGACCGGATCAACGCTTCTTCAAGAGTTTCAAGACAGCAG 1697
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Db 757 GTGACACGGGATCTGACGACCTGCGCAGCGGAGGGAGCGTGGGCTCCGGGAC 816
Qy 1518 TCCGACATGACATCACTCCAGACGATGCCATATCACTACGGGAACTCCGGGGACCA 1577
Db 817 TCCGACATGACATCACTCCAGACGATGCCATATCACTACGGGAACTCCGGGGACCA 876
Qy 1578 CTGGTAACCTGATGAGCGAGGCTATTGGCATCAACAGCTCAAGGTCAGCGGTGACATC 1637
Db 877 CTGGTAACCTGATGAGCGAGGCTATTGGCATCAACAGCTCAAGGTCAGCGGTGACATC 936
Qy 1638 TCCCTTGCATCCCTCAACCGCATCAACGCTTCTCAAGAGTTCCAAAGCAAGCAG 1697
Db 937 TCCCTTGCATCCCTCAACCGCATCAACGCTTCTCAAGAGTTCCAAAGCAAGCAG 996
Qy 1698 ATCAAAAGCTGGAAGAGCGCTTCAATCGGATACGATGGGACGATCAACCAACCTG 1757
Db 997 ATCAAAAGCTGGAAGAGCGCTTCAATCGGATACGATGGGACGATCAACCAACCTG 1056
Qy 1758 GTGGATGAGCTGAAGGCGACCAACCGGACTTCCAGAGGTGACAGTGAATTTATGTG 1817
Db 1057 GTGGATGAGCTGAAGGCGACCAACCGGACTTCCAGAGGTGACAGTGAATTTATGTG 1116
Qy 1818 CAAAGAGTTGCGCGCAATTCACCTTCTCAAGAGCGGATCCAGATGGTGAATCATC 1877
Db 1117 CAAAGAGTTGCGCGCAATTCACCTTCTCAAGAGCGGATCCAGATGGTGAATCATC 1176
Qy 1878 GTCAAGGTCAACGGGGGCTCTCTAGTGAATCGATGAGTGAAGAGCCGTGCTGACC 1937
Db 1177 GTCAAGGTCAACGGGGGCTCTCTAGTGAATCGATGAGTGAAGAGCCGTGCTGACC 1236
Qy 1938 GAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1997
Db 1237 GAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1296
Qy 1998 CCTGAGGTGATGATGAGGGGCGCATTCCTCCAGCGCCAGAGCTGAGCCCTGC 2052
Db 1297 CCTGAGGTGATGATGAGGGGCGCATTCCTCCAGCGCCAGAGCTGAGCCCTGC 1351

RESULT 14
US-09-796-858-9
; Sequence 9, Application US/09796858
; Patent No. US20020055139A1
; GENERAL INFORMATION:
; APPLICANT: Holtekmann, Douglas
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC,
; FILE REFERENCE: 7853-226-999
; PREVENTIVE, THERAPEUTIC, AND OTHER USES
; CURRENT APPLICATION NUMBER: US/09/796,858
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
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; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 50
; SEQ ID NO 9
; LENGTH: 1044
; TYPE: DNA
; ORGANISM: Mouse
; US-09-796-858-9

Query Match 32.4%; Score 975; DB 3; Length 1044;
Best Local Similarity 100.0%; Pred. No. 4.5e-272; Indels 0; Gaps 0;
Matches 975; Conservative 0; Mismatches 0;

Qy 1038 GGTCTCAACCACTGAGCAGCCCGGCTACAAAGTTCAATTGATGCTGACGTGTGAG 1097
Db 70 GGTCTCAACCACTGAGCAGCCCGGCTACAAAGTTCAATTGATGCTGACGTGTGAG 129
Qy 1098 AAGATCGACCAACCGGCTGCTCAATAGAGCTTCTTGAAGACACCCGCTGTTGGCGCG 1157
Db 130 AAGATCGACCAACCGGCTGCTCAATAGAGCTTCTTGAAGACACCCGCTGTTGGCGCG 189
Qy 1158 AAGTGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1217
Db 190 AAGTGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 249
Qy 1218 AATGCCAAGTGTGTCTCAAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1277
Db 250 AATGCCAAGTGTGTCTCAAGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 309
Qy 1278 CTACGAATGGGAGATCTCTATAGAGCCACATCAAAAGCATGTGAAGAGTGGACATT 1337
Db 310 CTACGAATGGGAGATCTCTATAGAGCCACATCAAAAGCATGTGAAGAGTGGACATT 369
Qy 1338 GCCACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTTGTTGTTGTTGTTGTTGTTGTT 1397
Db 370 GCCACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTTGTTGTTGTTGTTGTTGTTGTT 429
Qy 1398 GACCTGCGGCTGAGGAGTTGTGTGTGTCATGCGAGTCCCTTGCCTTACAGAACACA 1457
Db 430 GACCTGCGGCTGAGGAGTTGTGTGTGTCATGCGAGTCCCTTGCCTTACAGAACACA 489
Qy 1458 GTGAACAAGGAGATGTGACGATGCTGCCAGCGGAGGAGGAGGAGTCTGGGCTCCGGGAC 1517
Db 490 GTGAACAAGGAGATGTGACGATGCTGCCAGCGGAGGAGGAGGAGGAGTCTGGGCTCCGGGAC 549
Qy 1518 TCCGACATGAGTACATCAACGAGATGTCATCACTAAGGAACTCCGGGGACCA 1577
Db 550 TCCGACATGAGTACATCAACGAGATGTCATCACTAAGGAACTCCGGGGACCA 609
Qy 1578 CTGGTAACCTGATGAGCGAGGCTATTGGCATCAACAGCTCAAGGTCAGCGGTGACATC 1637
Db 610 CTGGTAACCTGATGAGCGAGGCTATTGGCATCAACAGCTCAAGGTCAGCGGTGACATC 669
Qy 1638 TCCCTTGCATCCCTCAACCGCATCAACGCTTCTCAAGAGTTCCAAAGCAAGCAG 1697
Db 670 TCCCTTGCATCCCTCAACCGCATCAACGCTTCTCAAGAGTTCCAAAGCAAGCAG 729
Qy 1698 ATCAAAAGCTGGAAGAGCGCTTCAATCGGATACGATGGGACGATCAACCAACCTG 1757
Db 730 ATCAAAAGCTGGAAGAGCGCTTCAATCGGATACGATGGGACGATCAACCAACCTG 789
Qy 1758 GTGGATGAGCTGAAGGCGACCAACCGGACTTCCAGAGGTGACAGTGAATTTATGTG 1817
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Db 790 GTGATGAGCTGAGAGCCAGCAACCCGGACTTCCAGAGGTGAGCAAGTGAATTTATGTC 849
Qy 1818 CAAGAGTTGGCCGCAATTCCTTCTGAGAGAGGGGCGATCCAGATGGTATGATCATC 1877
Db 850 CAAGAGTTGGCCGCAATTCCTTCTGAGAGAGGGGCGATCCAGATGGTATGATCATC 909
Qy 1878 GTCAAGGTCAACGGGCGTCTCTAGTGAAGTCTGAGTGAAGCTGAGAGGCGTGTGACC 1937
Db 910 GTCAAGGTCAACGGGCGTCTCTAGTGAAGTCTGAGTGAAGCTGAGAGGCGTGTGACC 969
Qy 1938 GAGTCTCTCTCTCTCTGAGAGGTGCGCGGGGAAAGAGAGCTCTCTTCAAGCATCGCA 1997
Db 970 GAGTCTCTCTCTCTCTGAGAGGTGCGCGGGGAAAGAGAGCTCTCTTCAAGCATCGCA 1029
Qy 1998 CCTGAGGTGTCATG 2012
Db 1030 CCTGAGGTGTCATG 1044

RESULT 15

US-10-485-313A-26
; Sequence 26, Application US/10485313A
; Publication No. US2005005902A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiying
; APPLICANT: SALAMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent version 3.1
; SEQ ID NO 26
; LENGTH: 2450
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-485-313A-26

Query Match 27.5%; Score 825.2; DB 9; Length 2450;
Best Local Similarity 68.9%; Pred. No. 1.8e-228;
Matches 1365; Conservative 0; Mismatches 543; Indels 74; Gaps 14;

Qy 1034 CGCAGGTCTCCACGAGCTGAGAGCGCGGCTACAAAGTTCACTTCTGAGAGTGT 1093
Db 525 CTCTGCTCTCCACGAGCTGAGAGCGCGGCTACAAAGTTCACTTCTGAGAGTGT 584
Qy 1094 GGAAGAGATGCGACGAGCGGTGTCCACATAGAGCTTCTCTGAGAGACCGGCTGTTGG 1153
Db 585 GGAAGAGATGCGACGAGCTGTGTCTCACATAGAGCTTCTCTGAGAGACCGGCTGTTGG 644
Qy 1154 CCGCAACGTGCCCTGTCTCAGCGGTTCTGGCTTCAATGATGAGAGCGCGGCTGATCAT 1213
Db 645 CCGGATGTGCGCTGTCTCAGTGGCTCGGGCTTCAATGATGAGAGCGGCTGATCAT 704
Qy 1214 CACCAATGCCACGTTGTCTCAGCAAGTGTGTCGCCCGGCGAGGAGAGCTCAAGT 1273
Db 705 CACCAATGCCACGTTGTCTCAGCTTCCAGCACTGCTCCGCGCGAGAGCTCAAGT 764
Qy 1274 GCAAGTACAGATGGGGAATCTCTATAGGCGCACATCAAGATGCAAGAGTCCGA 1333
Db 765 GCAAGTACAGATGGGGAATGCTTATAGGCGCACATCAAGATGCAAGAGTCCGA 824
Qy 1334 CATTCGCAACATCAAGATTCATCCCAAGAAAAGCTCCCTGTGTGTGTTGCTGGTCACTC 1393
Db 825 CATTCGCAACATCAAGATTCATCCCAAGAAAAGCTCCCTGTGTGTGTTGCTGGTCACTC 884

Qy 1394 GGCACCTGCGCGCTGGGAGATTTGTGTGTCATTCGCACTGCCCTTCCGCTACAGAA 1453
Db 885 AGCACAACCTGCGCGCTGGGAGATTTGTGTGTCATTCGCACTGCCCTTCCGCTACAGAA 944
Qy 1454 CACAGTGAACAGGCGATGTCAGACATGCGCCAGCGGAGGCGAGGAGCTGGGCTCCG 1513
Db 945 CACCGTGAACAGGCGATGTCAGACATGCGCCAGCGGAGGAGGAGGAGCTGGGCTCCG 1004
Qy 1514 GGAAGTCCGACATGACATTCACAGAGGATGCGCATTCATCACTACGAGAACTCCGAGG 1573
Db 1005 GGAAGTCCGACATGACATTCACAGAGGATGCGCATTCATCACTACGAGAACTCCGAGG 1064
Qy 1574 ACCAATGTAAGCTGATGAGGAGTATGAGATGAGATGAGATGAGATGAGATGAGAT 1633
Db 1065 ACCCGTGAACCTGATGAGGAGGATGAGATGAGATGAGATGAGATGAGATGAGAT 1124
Qy 1634 CATCTCTTTGTCATCCCTCAGACCGCATCAACGTTCTCTCAAGATTCGAAGCAA 1693
Db 1125 CATCTCTTTGTCATCCCTCAGATCGATCAACGTTCTCTCAAGATTCGAAGCAA 1184
Qy 1694 GCAAGTCAAGAGCTGAGAGAGGCGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1753
Db 1185 GCAAGTCAAGAGCTGAGAGAGGCGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1244
Qy 1754 CCGTGTGATGAGTGAAGGCGCAAGCCGAGCTTCCAGAGATCAGAGTGAATTTA 1813
Db 1245 TTTGATGAGAGATGAGAGGCGCGCAACCCAGATTTTCAAGGAGTGAATTTA 1304
Qy 1814 TGTGCAAGAGTTGCGCGCAATTCATCTTCAAGAGGCGGATTCAGAGTGAATTTA 1873
Db 1305 TGTGCAAGAGTTGTTCCCAATTCATCTTCAAGAGGAGGAGGAGGAGGAGGAGGAG 1364
Qy 1874 CATCTCAAGTGAACGAGCGCTCTCTGATGAGATGAGTGAAGTGAAGGAGGAGGAG 1933
Db 1365 CATCTCAAGTGAACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1424
Qy 1934 GACGAGTCT 1993
Db 1425 GACGAGTCT 1484
Qy 1994 GGCACCTGAGGTGTCTATGAGGAGGCGCATTCCTTCAAGCGGCAAGCGTCAAGGCTGCA 2053
Db 1485 CATCTCTGAGGTGTCTATGAGGAGGCGCATTCCTTCAAGCGGCAAGCGTCAAGGCTGCA 1541
Qy 2054 GACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2113
Db 1542 GAAAGTGGGAGTTCGCGCGCTTCAATGAAATCAAGGAGGAGGAGGAGGAGGAGGAGGAG 1600
Qy 2114 GGGCGGAGCGCT 2173
Db 1601 GATCAACAGTCT 1660
Qy 2174 GCAATTTCCGCTGGGAGGAGTGTGATCAATCCGAGTCCGAGGAGGAGGAGGAGGAGGAG 2233
Db 1661 CGGATCTAGCG-----TGAACCTTAATTTCACTCAAGTGAAGGAGGAGGAGGAGGAG 1711
Qy 2234 TCCCTTGAAGATGATCTGAAAGTCACTTCAAGTCTTCCGATTTTCAAAATCTG 2293
Db 1712 TCCCTTGAAGATGATCTGAAAGTCACTTCAAGTCTTCCGATTTTCAAAATCTG 1771
Qy 2294 C---CTTCATGAGAGTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2350
Db 1772 GAAATCTCTGAAAGTGTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1831
Qy 2351 ATCTGCAATATCCCTGCT 2410
Db 1832 CAGGAAGGCGACCGGCTCCCATCCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1891
Qy 2411 CCCCTGAACAAAGCGGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2470
Db 1892 TCTCTCTGTCAGGAGCTTCTCTGACATCAAGGCTTCTCTCTCTCTCTCTCTCTCTCTCT 1951
Qy 2471 AAGCT---GTAAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2525

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 21, 2006, 19:00:15 ; Search time 806 Seconds

(without alignments)
7917.093 Million cell updates/sec

Title: US-10-617-443b-1

Perfect score: 3006
Sequence: 1 caggagactcgaagtttcag.....gccaaaaaaaaaaaaaaaa 3006

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_New:*

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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RefAlt	Score	Query	Match	Length	DB	ID	Description
1783	59.3	2551	12	US-11-186-284-78	Sequence 78, Appl		
2	385	12.8	1443	8	US-10-821-234-613	Sequence 613, App	
3	385	12.8	1894	9	US-11-072-512-795	Sequence 795, App	
4	385	12.8	2036	12	US-11-091-883-91	Sequence 91, Appl	
5	290.6	9.7	2476	12	US-11-183-914-23	Sequence 23, Appl	
6	130.2	4.3	908	8	US-10-750-185-32084	Sequence 32084, A	
7	130.2	4.3	908	8	US-10-750-623-32084	Sequence 32084, A	
8	81.6	2.7	1497	8	US-10-467-657-2095	Sequence 2095, Ap	
9	66.2	2.2	1446	8	US-10-454-437-55	Sequence 55, Appl	
10	62	2.1	1376	8	US-10-750-185-32073	Sequence 32073, A	
11	62	2.1	1376	8	US-10-750-623-32073	Sequence 32073, A	
12	56.2	1.9	577	6	US-09-925-065A-873761	Sequence 873761, A	
13	54.8	1.8	1102	8	US-10-750-185-32074	Sequence 32074, A	
14	54.8	1.8	1102	8	US-10-750-623-32074	Sequence 32074, A	
15	53.4	1.8	586	6	US-09-925-065A-873523	Sequence 873523, A	
16	52.4	1.7	199321	12	US-11-121-086-10	Sequence 10, Appl	
17	52.2	1.7	649	6	US-09-925-065A-946511	Sequence 946511, A	
18	52.2	1.7	651	6	US-09-925-065A-949922	Sequence 949922, A	
19	51.8	1.7	649	6	US-09-925-065A-921371	Sequence 921371, A	
20	51.8	1.7	651	6	US-09-925-065A-928800	Sequence 928800, A	

21	49.6	1.7	595	6	US-09-925-065A-829367	Sequence 829367, A
22	49.6	1.7	601	6	US-09-925-065A-766718	Sequence 766718, A
23	47.8	1.6	597	6	US-09-925-065A-907102	Sequence 907102, A
24	47.8	1.6	637	6	US-09-925-065A-74401	Sequence 74401, A
25	47.6	1.6	440	6	US-09-925-065A-257729	Sequence 257729, A
26	47.6	1.6	588	6	US-09-925-065A-920930	Sequence 920930, A
27	46.4	1.5	440	6	US-09-925-065A-257728	Sequence 257728, A
28	46.2	1.5	609	6	US-09-925-065A-816217	Sequence 816217, A
29	46.2	1.5	609	6	US-09-925-065A-816218	Sequence 816218, A
30	46.2	1.5	2849	9	US-11-072-512-436	Sequence 436, App
31	45.8	1.5	579	6	US-09-925-065A-118576	Sequence 118576, A
32	45.8	1.5	1992	6	US-09-925-065A-208590	Sequence 208590, A
33	45	1.5	497	6	US-09-925-065A-816219	Sequence 816219, A
34	45	1.5	609	6	US-09-925-065A-534251	Sequence 534251, A
35	45	1.5	609	6	US-09-925-065A-669549	Sequence 669549, A
36	43.8	1.5	525	6	US-09-925-065A-168630	Sequence 168630, A
37	43.4	1.4	722	6	US-09-925-065A-45901	Sequence 45901, A
38	43.2	1.4	8888	7	US-10-933-746-41	Sequence 41, Appl
39	43.2	1.4	544	6	US-09-925-065A-45902	Sequence 45902, A
40	43	1.4	544	6	US-09-925-065A-45903	Sequence 45903, A
41	43	1.4	544	6	US-09-925-065A-669171	Sequence 669171, A
42	43	1.4	624	6	US-11-121-086-28	Sequence 28, Appl
43	43	1.4	172111	12	US-11-072-512-1144	Sequence 1144, Appl
44	43	1.4	3354	9	US-11-072-512-1144	Sequence 1144, Appl
45	42.8	1.4	3354	9	US-11-072-512-1144	Sequence 1144, Appl

ALIGNMENTS

RESULT 1
US-11-186-284-78

Sequence 78, Application US/1186284
Publication No. US2005026493A1

GENERAL INFORMATION:

APPLICANT: Millennium Pharmaceuticals, Inc.

APPLICANT: Berger, Allison

APPLICANT: Guillemette, Tracy L.

APPLICANT: Kamackar, Shubhangi

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John B.

APPLICANT: Thibodeau, Stephen N.

APPLICANT: Burgart, Lawrence J.

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND

TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

FILE REFERENCE: MPM01-029P2RNM

CURRENT APPLICATION NUMBER: US/11/186,284

PRIOR FILING DATE: 2005-07-21

PRIOR FILING DATE: 2002-11-21

PRIOR FILING DATE: 2001-12-10

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2002-05-20

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 78

LENGTH: 2551

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (222) ... (1580)

US-11-186-284-78

Query Match

Best Local Similarity

Matches 1928; Conservative

Score 1783; DB 12; Length 2551;

Pred. No. 0; Gaps 12;

Indels 16; Gaps 12;

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Db 606 GGCTCCACACAGCTGAGACAGCCGCGCTACAACTTCACTTCTGACGTGGAG 665
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Qy 1098 AAGATGCAACAGCCGTGTGTCATAGAGCTTCTCTGAGAACCCGCTGTTGGCCG 1157
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Db 666 AAGATGCAACAGCCGTGTGTCATAGAGCTTCTCTGAGAACCCGCTGTTGGCCG 725
|||
Qy 1158 AACGTCCCTGTGTCAGAGGTTCTGCTTCAATGATGACAGAGCCGCTGATCATCC 1217
|||
Db 726 AACGTCCCTGTGTCAGAGGTTCTGCTTCAATGATGACAGAGCCGCTGATCATCC 785
|||
Qy 1218 AATGCCACGTGTGTCAGAACAGTGTGCTCCCGGAGAGGAGCAAGTCAAGTTCAG 1277
786 AATGCCACGTGTGTCAGAACAGTGTGCTCCCGGAGAGGAGCAAGTCAAGTTCAG 845
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Qy 1278 CTACAAATGAGGATCTCTATAGAGGACCAATGAAGATGCAAGAAAGTGGACAT 1337
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Db 846 CTACAAATGAGGATCTCTATAGAGGACCAATGAAGATGCAAGAAAGTGGACAT 905
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Qy 1338 GCCACATCAAGATCCATCCCAAGAAAAGCTCCTGTGTGTGTGCTGGGTCACTGGCC 1397
906 GCCACATCAAGATCCATCCCAAGAAAAGCTCCTGTGTGTGTGCTGGGTCACTGGCC 965
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Qy 1398 GACCTGCGCTGGGAGTTGTGTGGCCATGCAATGCTCCCTGCTTACAGAACCA 1457
966 GACCTGCGCTGGGAGTTGTGTGGCCATGCG-AGTCCCTTCCGCTTACAGAACCA 1023
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Qy 1458 GTGACAAAGGAGCTGTCAGACATGCGCAGCGGAGGAGGAGTGGGCTCCGAGAC 1517
1024 GTGACAAAGGAGCTGTCAGACATGCGCAGCGGAGGAGTGGGCTCCGAGAC 1080
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Qy 1518 TCCGACATGAGATCAAT-CCAGAGGATGCAAT-CAACTGAGGAACTCCGAGGAGAC 1575
1081 TCCGACATGAGATCAAT-CCAGAGGATGCAAT-CAACTGAGGAACTCCGAGGAGAC 1140
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Qy 1576 CACTGTGAACCTGATGCGAGGATGATGATGATGATGATGATGATGATGATGATG 1635
1141 CACTGTGAACCTGATGCGAGGATGATGATGATGATGATGATGATGATGATGATG 1200
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Qy 1636 TCTCCTTTCGCAATCCCTGAGACCGGATGATGATGATGATGATGATGATGATGATG 1695
1201 TCTCCTTTCGCAATCCCTGAGACCGGATGATGATGATGATGATGATGATGATGATG 1260
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Qy 1696 AGATCAAGAGCTGAGAGGAGGCTTCTGATGATGATGATGATGATGATGATGATGATG 1755
1261 AGATCAAGAGCTGATGAGAGGCTTCTGATGATGATGATGATGATGATGATGATGATG 1320
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Qy 1756 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1815
1321 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
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Qy 1816 TGCAGAGGTTGCGAGAAATTCATCTTCAAGAGGAGGAGGATGAGAGGATGAGAGGATG 1875
1381 TGCAGAGGTTGCGAGAAATTCATCTTCAAGAGGAGGAGGATGAGAGGATGAGAGGATG 1440
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Qy 1876 TGTCAAGGTCAACGAGGCTCTCTAGTGAATGATGATGATGATGATGATGATGATGATG 1935
1441 TGTCAAGGTCAACGAGGCTCTCTAGTGAATGATGATGATGATGATGATGATGATGATG 1500
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Qy 1936 CCGAGTCT 1995
1501 CCGAGTCT 1560
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Qy 1996 CACCTGAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2055
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Qy 2056 CAACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2115
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Qy 2116 GCGGACGCT 2175
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Db 1680 GCGTCA--CTCTCTCTGCTGTCCGAGGAGCA--GGAGAGTGGGCTTGGC--AGGAGCG 1733
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Qy 2176 AATTCCGCTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2235
1734 AATTCCGCTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1793
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Qy 2236 CCGTGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2295
1794 CCGTGTACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1853
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Qy 2296 TTTCAATGAGAGTCCCT 2355
1854 TTTCAATGAGAGTCCCT 1913
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Qy 2356 CAGTATCCCTGCT 2415
1914 CAGTATCCCTGCT 1973
|||
Qy 2416 TGACAAAGCCCACTGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2475
1974 TGACAAAGCCCACTGACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2033
|||
Qy 2476 GTAGG 2535
2034 GTAGG 2093
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Qy 2536 CTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2594
2094 CTTTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2153
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2213 GGGAGG 2272
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Qy 2715 GGGAGG 2774
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Qy 2895 GTAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2954
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Qy 2955 GGAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2993
2513 GGAATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2551
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RESULT 2
US-10-821-234-613
; Sequence 613, Application US/10821234
; Publication No. US2005025511A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047

PRIOR FILING DATE: 2003-04-07
 NUMBER OF SEQ ID NOS: 1704
 SOFTWARE: pc_seq_genes Version 1.0
 SEQ ID NO 613
 LENGTH: 1443
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-821-234-613

Query Match 12.8%; Score 385; DB 8; Length 1443;
 Best Local Similarity 63.8%; Pred. No. 2.2e-81;
 Matches 630; Conservative 0; Mismatches 330; Indels 27; Gaps 2;

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 QY 1087 ACGTGTGAGAGATCCGACCGAGCGGTGTCACATAGAGCTCTTCTGAGACCCGC 1146
 DB 521 ACGTGTGAGAGATCCGCGCTGCGGTTCATATGGAATTTGTTGCAAGCTTCGT 580
 QY 1147 TGTTCGCGCAAGTCCCTGTCAGCGGTTCTGCTTCAATGTCAGAGCCGCGC 1206
 DB 581 TTTTAAACGAGAGGTGCGGAGGTGCTAGAGGCTGCTGTTTATGTGTGGAAGATGAC 640
 QY 1207 TGATCATCAACCAATGCCACCGTGTGTCCAGAACAGTGTCTGCCCGGAGCGACGC 1266
 DB 641 TGATGTGCAAAATGCCACGTGTGACCAAA-----GCACCGGG 682
 QY 1267 TCAAGTGCAGCTTACAGAAATGGGAGCTCTATGAGGCCCACTCAAGACATGACAAGA 1326
 DB 683 TCAAGTGTGAGTGAAGAGAGGTGCACTTAAAGAACCAATCAAGATGTGATGAGA 742
 QY 1327 AGTGGACATTTGCCACCATCAAGATCCATCCAGAAAAAGTCCCTGTGTTGCTGG 1386
 DB 743 AAGCAGACATGSCACTCAAAATTGACCAACAGGCGCAAGCTGCTGCTGCTGG 802
 QY 1387 GTCACTCGGCGCACTGCGGCGCTGGGAGTTGTGTGGCCATCGGAGTCCCTCGCC 1446
 DB 803 GCGGCTCTCTCAAGCTGCGGCGGAGATTGTGTGCGCATCGAAACCCGTTTCCC 862
 QY 1447 TACAGAACACAGTGAACAAGGCGATGTGAGCACTGCCAGGCGGAGGAGGAGAGCTG 1506
 DB 863 TTCAAAACACATCCACACCGGAGATGTGAGCAACCCAGGAGGCGCAAGAGCTG 922
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 DB 923 GCGTCCGCAACTCAAGCATGACTATCAACAGCGCATCACTATGGAAT 982
 QY 1567 CCGGGGAGCACTGTGTAACCTGAGTGGAGGTCATTTGGCATCAACAGCTCAAGTCA 1626
 DB 983 CCGGAGGCGCGTTAATGAACCTGAGCGGTAAGTGAATTAACATTTGAAAGTGA 1042
 QY 1627 GCGGTGCACTCTTGTGCATCCCTCGACCGCATCAAGGTTCTCCACAGAGTTCC 1686
 DB 1043 CAGCTGGAATCTCTTTGCAATCCATCTGAATGAATTAAGTTCTCCAGAGTCCC 1102
 QY 1687 AAGACAGAGATCAAG-----ACTGGAAGAGGCGTTCATCGGCATACGAGATC 1737
 DB 1103 AAGACAGAGGCGCAAGGAAAAAGCATCAACAGAAAGATATATGTATCCGAATGA 1162
 QY 1738 GGAAGATCAACCAAGCTGTGTGAGTGAAGCCAGCAACCCGAGCTTCCAGAG 1797
 DB 1163 TGTCACTCACTGTCAGCAAGGCAAGAGCTGAAGAGCGGAGCTTCCAGAG 1222
 QY 1798 TCAGAGTGAATTTATGTGAAGAGTTCGCGCAATTCACCTTCTCAGAGAGCGGCA 1857
 DB 1223 TGAATCAGAGAGATATTAATTAAGTAAATTCCTGATACCCAGAGAGAGCTGGTTC 1282
 QY 1858 TCCAAAGTGTGATCATGTCAGAGTCAACGAGGCTCTTATGAGACTGAGTGAAC 1917
 DB 1283 TCAAGGAAAAAGACGTATATCAGATCAATGAGCAGTCCGTGTGCTCCGCAATGATG 1342

QY 1918 TGACAGAGCGCGTGTGACCGAGTCTCTCTCTACTGAGAGTGGCGGAGAACGAG 1977
 DB 1343 TCAGCAGCTATTTAAAGGAAAGCAACCTGGAACATGTGTGTCCGAGGGGTATAGAG 1402
 QY 1978 ACTCTCTTTCAGCATGCACTGAGG 2004
 DB 1403 ATATCATGATCATCAGTATTCGGAAG 1429

RESULT 3

US-11-072-512-795
 Sequence 795, Application US/11072512
 Publication No. US20060029945A1

GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
 APPLICANT: SUGIYAMA, TOMOYASU
 APPLICANT: OTSUKI, TETSUJI
 APPLICANT: WAKAMATSU, AI
 APPLICANT: SATO, HIROYUKI
 APPLICANT: ISHII, SHIZUKO
 APPLICANT: YAMAMOTO, JUN-ICHI
 APPLICANT: ISONO, YUUKO
 APPLICANT: HIO, YURI
 APPLICANT: OTSUKA, KAORU
 APPLICANT: NAGAI, KEIICHI
 APPLICANT: IRIE, RYOTARO
 APPLICANT: TAMECHIKA, ICHIRO
 APPLICANT: SEKI, NAOHIKO
 APPLICANT: YOSHIIKAWA, TSUTOMU
 APPLICANT: OTSUKA, MOTOYUKI
 APPLICANT: NAGAHARI, KENJI
 APPLICANT: MASUHO, YASUHIKO
 TITLE OR INVENTION: Novel full length cDNA
 FILE REFERENCE: 084335-0191
 CURRENT APPLICATION NUMBER: US/11/072, 512
 PRIOR FILING DATE: 2005-03-07
 PRIOR APPLICATION NUMBER: US 60/350, 978
 PRIOR FILING DATE: 2002-01-25
 PRIOR APPLICATION NUMBER: JP 2001-379298
 NUMBER OF SEQ ID NOS: 4096
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 795
 LENGTH: 1894
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-11-072-512-795

Query Match 12.8%; Score 385; DB 9; Length 1894;
 Best Local Similarity 63.8%; Pred. No. 2.4e-81;
 Matches 630; Conservative 0; Mismatches 330; Indels 27; Gaps 2;

QY 1027 CCGCCAGGCGAGTCTCCACAGCTGAGACCGCGGCTACAAAGTTCAACTTCTG 1086
 DB 364 CCGGCGCAAGGAGGAGAAATCCCAAGTTTGGCCATTAATTAATTTATCGGG 423
 QY 1087 ACGTGTGAGAGATCCGACCAAGCGGTGTGCAATAGAGCTCTTCTGAGACCCGC 1146
 DB 424 ACGTGTGAGAGATCCGCGCTGCGGTTCATATGAATTTGTTGCAAGCTTCGT 483
 QY 1147 TGTTCGCGCAAGTCCCTGTCAGCGGTTCTGCTTCAATGTCAGAGCGGCGC 1206
 DB 484 TTTCTAAACGAGAGGTGCGGTGCTATGTGGTCTGGTTTATGTGTGGAAGATGAC 543
 QY 1207 TGATCATCAACCAATGCCAGGTGTGTCCAGCAAGTGTGCCCCGAGGAGCGACGC 1266
 DB 544 TGATGTGCAAAATCCACGAGGTGACCAAA-----GCACCGGG 585
 QY 1267 TCAAGTGCAGCTTACAGAAATGGGAGCTCTATGAGGCCACATCAAGACATGACAAGA 1326
 DB 586 TCAAGTGTGAGTGAAGAGGTGCACTTACGAAGCCAAATCAAGATGTGATGAGA 645
 QY 1327 AGTGGACATTTGCCACCATCAAGATCCATCCAGAAAAAGTCCCTGTGTTGCTGG 1386

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Db      646 AAGCAGCATTCGACATCATAAATTGACACACGAGGCAAGCTGCTCTGCTGCTTGG 705
QY      1387 GTCACTCGGCGGACCTCGGCGCTTGGGAGATTGTGTGGCCATCGGCAATCCTTGGCCC 1446
Db      706 GCGCGCTCTCAAGAGCTGCGCGCCGAGAGATTGCTGTGCTCGCAATCGGAAGCCCTTTTCCC 765
QY      1447 TACAGAACACAGTGAACAAGGAGCATGTCAGCACTGCCACGAGGAGGAGGAGGAGCTG 1506
Db      766 TTCAAAACACAGTACACACCGGAGTGTGAGCACACCCAGGAGGCGGCAAGAGCTGG 825
QY      1507 GCCTCGGAGACTTCGACATGAGCTACATCGAGCGGATCGCATCAACTACGAGAACT 1566
Db      826 GGCCTCGCAATCTCAGCATGAGCTACATCAGACCGACGCAATCACTAATAGAACT 885
QY      1567 CCGGAGGAGCAGCTGTGAACTTGGATGGGAGGTCAATGGCATCAACAGCTCAAGTCA 1626
Db      886 CCGGAGGCGCGTTAGTAACTTGAACGCTGAGAGTGAATTTGAATTAACATTTGAAAGTGA 945
QY      1627 CCGGCTGCAATCTCTTGGCATCCCTCAGACCGCATCAAGGTTCTCAGAGAGTTGC 1686
Db      946 CAGCTGGAATCTCTTTTGCATCTCCATCTGATTAAGTTAAAGTTCTCTCAGGAGTCCC 1005
QY      1687 AAGACAGCAGATCAAAAG-----ACTGGAAGAGCGCTTCATCGGCATACGAGTGC 1737
Db      1006 ATGACCGACAGGCGCAAGGAAAGCCATCACCAAGAAAGATTAATGGATCCGAAATGA 1065
QY      1738 GGAACATCAACCAAGCGCTGTGTGATGATGATGAGGCGAGCAACCGGCACTTCCAGAG 1797
Db      1066 TGTCACTCACTGCTCAGCAAAAGCCAAAGAGCTGAAGAGCCGAGCACTTCCAGAG 1125
QY      1798 TCAGCAGTGAATTTATGTGCAAGAGGTTGCGCGCAATTCACCTTCTCAGAGAGCGGCA 1857
Db      1126 TGATCTCAGAGAGGCTATTAATTAATGAAGTAATTTCTTAATACCCAGAGAGCTGTGTC 1185
QY      1858 TCCAGATGATGACATCATCTGTCAGAGTCAACGAGGCGCTCTTAATGAGCTCGAGTGC 1917
Db      1186 TCAGGAAAAACGACGCTATATATCAGATCAATGAGACAGTCCGAGTCTCGCAATGAG 1245
QY      1918 TGCAGAGGCGCTGTGACCGAGCTCTCTTCTTACTGAGAGTGGCGGCGGAGAGAG 1977
Db      1246 TAGCGACGCTATTAAGGAAAGCACTGAAACATGTGTGTCGCAAGGCTAATGAAG 1305
QY      1978 ACCTCCTTTCAGCATCGACCTGAGG 2004
Db      1306 ATATCATATCATCAGTGAATCCGGAAG 1332

RESULT 4
US-11-091-883-91
; Sequence 91, Application US/11091883
; Publication No. US20060024693A1
; GENERAL INFORMATION:
; APPLICANT: CIBELLI, JOSE
; APPLICANT: FERNANDEZ, EMILIO O.
; APPLICANT: JORDAO DE MEGALHAES, GUILHERME
; APPLICANT: KOCABAS, ARIF
; APPLICANT: CROSBY, JAVIER A.
; TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
; TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEBORN
; FILE REFERENCE: 53942US
; CURRENT APPLICATION NUMBER: US/11/091,883
; PRIOR FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: 60/556,875
; NUMBER OF SEQ ID NOS: 513
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91
; LENGTH: 2036
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-091-883-91

```

```

Query Match      12.8%; Score 385; DB 12; Length 2036;
Best Local Similarity 63.8%; Pred. No. 2,4e-81;
Matches 630; Conservative 0; Mismatches 330; Indels 27; Gaps 2;

QY      1027 CCGCAGCGCAGGTGTCCACGAGCTGAGACGCCGCGCTACAAAGTTCAACTTCAATGCTG 1086
Db      509 CTTGGGCGCAAGGGCAGAGAAAGATCCCAACAGTTTCCGCCATTAATATACTTATTCGCGG 568
QY      1087 AGTGTGGAAGAAATGCCAACCAAGCGGTGTCCACATAGAGTCTTCTGAGACACCCGC 1146
Db      569 AGTGTGGAAGAAATGCCCGCTGCGGTTCATATGAAATGTTTGGCAAGCTTCCGT 628
QY      1147 TGTTCGCGCGCAAGCTGCGCCCTGTCCAGCGGTTTGTGCTTCATATGTCAGAGCGCGC 1206
Db      629 TTTCTTAAACGAGAGGTGCGGTGCTGATGAGGTCTGTGGTTTATTTGTGCGAAGATGAC 688
QY      1207 TGATCATCAACCAATGCCACGTTGTGTCCAGCAACAGTGTGCCCCGAGCAGCAGAC 1266
Db      689 TGATGTGCAAAATGCCACGTTGTGACCAAA-----GCACCGGG 730
QY      1267 TCAGGTGAGCTTAAGAAATGGGAGCTCTATAGAGCCCACTAAAGACATCGACAAAG 1326
Db      731 TCAGAGTTGAGCTGAAGAACGCTGCCTTAAGAAAGCCAAATTAAGATGTGATGAGA 790
QY      1327 AGTCGACATTCGACATCAAGATCCCAAGAAAAAGCTCCCTGTGTGCTGG 1386
Db      791 AAGCAGACATCGCATCTCAATAAATTGACACACAGGCGAGAGTGTCTGTCTGCTTGG 850
QY      1387 GTCACTCGGCGCAGCTGTGGGCTTGGGAGATTGTGTGGCCATTCGCAAGTCTTCCGCC 1446
Db      851 GCGGCTCTCAGAGGCTGCGGCGGAGAGTTCTGTGTGCGCATTCGGAAGCCGTTTCCC 910
QY      1447 TACAGAACACAGTGAACAAGGCACTGTACAGACTGCCCCAGGGAGGCGAGGAGCTGG 1506
Db      911 TTCAAAACACAGTCAACACCGGAGTGTGAGACCAACAGAGAGGCGGCAAGAGCTGG 970
QY      1507 GCCTCGGAGCTCCGACATGGACTACATCCAGACGAGTGCATCATCACTCGGAACT 1566
Db      971 GCTCTCGCAATCTCAAGATGAGCTATCAGACCGAGCCATCTCAACTATGAAACT 1030
QY      1567 CCGGAGGACCACTGTGTGAACCTGATGGCGAGGTGATTTGGATCAACGCTCAAGTCA 1626
Db      1031 CCGGAGGCGCGTTAGTAACCTGAGCGGTGAAGTGAATTAACAATTGAAAGTGA 1090
QY      1627 CCGGCTGCAATCTCTTGGCCATCCCTCAGACCGGATCAACAGGTTCTCTACAGAGTCC 1686
Db      1091 CAGCTGGAATCTCTTGCATCCATCTGATTAAGATTAAAGTTCTCTCAGAGGTCCC 1150
QY      1687 AAGCAGCAGATCAAAAG-----ACTGGAAGAGCGCTTCATCGGCATACGAGTGC 1737
Db      1151 ATGACCGACAGGCGCAAGGAAAGCAATCACCAAGAAAGATTAATTTGTATCCAAATGA 1210
QY      1738 GGAACATCAACCAAGCTGTGATGAGCTGAAGGCGACCAACCCGAGCTTCCAGAGG 1797
Db      1211 TGTCACTACGCTCAGCAAAAGCAAAAGCTGAAGAGCCGAGCAGGAGCTTCCAGAG 1270
QY      1798 TCAGCAGTGAATTTATGTGCAAGAGTTGGCGCCCAATTCACCTTCTCAGAGAGCGGCA 1857
Db      1271 TGATTTCAAGAGCGGTATTAATTAATGAAGTAATTTCTGATACCCACAGAAAGCTGTGTC 1330
QY      1858 TCCAGATGATGACATCATCTGCAAGGTCAACGAGGCGTCTCTAATGAGACTGAGTGC 1917
Db      1331 TCAGGAAAAACGACGCTATTAATCAGATCAATGAGCAAGTGTGTCTTCCGCAATGAG 1390
QY      1918 TGCAGAGGCGCTGTGACCGAGTCTCTCTTAAGAGTGGCGGCGGAGAGAGAG 1977
Db      1391 TCAGGAGGTATTAAGGAAAGCAACCTGGAACATGAGTGTGTCGAGGAGGTAATGAAG 1450
QY      1978 ACCTCCTTTCAGCATCGACCTGAGG 2004
Db      1451 ATATCATATCATCAGTGAATCCGGAAG 1477

```

RESULT 5
US-11-183-914-23
Sequence 23, Application US/11183914
Publication No. US2005028214A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Tang, Tom Y.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/183,914
FILING DATE: 19-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINITUCT01
CLONE: 2680548
US-11-183-914-23

Query Match 9.7%; Score 290.6; DB 12; Length 2476;
Best Local Similarity 57.6%; Pred. No. 5.7e-59;
Matches 577; Conservative 0; Mismatches 394; Indels 30; Gaps 2;

QY 1017 CTGGCCCTTCCCGCAGCGCTCCACCACTGAGCGCCGCGCTTACAGTTCAAC 1076
DB 445 CCGGCGCTCTCGCGCGCTCCCTAGCCGCGCGCTTCTCCCGAGTCAAGTCAAC 504
QY 1077 TTCAATGCTGAGTGTGGAAGAATCGACAGCCGCTGCTCACTAGAGCTTTCTCG 1136
DB 505 TTCAATGCTGAGTGTGGAAGAAGACAGACCTCGCTGCTTATATCAAGATCTCGAAC 564
QY 1137 AGACACCGCGCTGTTGGCCGCAACGTGCGCTGTCAGGCGTTCTGGCTTCAATGATCA 1196
DB 565 CGGACACCTTTTCTGGCGCGCGAGTCCCTATCTGAAAGCGCTCAGAGATTCTGTGGCT 624
QY 1197 GAGCGCGCGCTGATCATCAACCAATGCCACGCTGTGTCTCAGCAAGTGTCTCCCGGCG 1256
DB 625 GCCGATGGGCTCATGTGTCAACCAAGCCCATGTGTG-----GCTGAT 666

QY 1257 AGGCAGACCTCAAGTGTACAGTACAGATGGGGACTCTCTATGAGGCCACATCAAGAC 1316
DB 667 CGGCGCAGAGTCCGTGTGAGACTGTAAAGCGCGCAGCATAGAGCCGTGTCAACAGT 726
QY 1317 ATCGACAAGAAAGTCCGACATTTGCCACCATCAAGATCAATCCCAAGAAAAAGCTCCCTGTG 1376
DB 727 GTGATTCCTCGTGTGAGACATGCGAACGCTAGAGATTTAGACTTAAGAGGCTCTCCCAAG 786
QY 1377 TTGTTGCTGGGTCACTCGGCGGACTGTGGGAGTTGTGTGCTCATCGGCACT 1436
DB 787 CTGCTCTGGGACGCTCAGCTGATGTCCGGGAAGGGAGTTGTGTGCTCATGGGAAGT 846
QY 1437 CCTTGCCCTTACAGAACAGTGAACAAGGCAATGTCAGACTGCCAGCGGAGGAGGCG 1496
DB 847 CCTTTGACCTGCAACACATCAATCCGCACTGTTAGCTGTGCTCAAGCTCAAGC 906
QY 1497 AGGAGCTGGGCTCCGGAACCTCGACATGACTATCCAGACGAGATCCATCAATCAAC 1556
DB 907 AGAGACTGGGACTCCCAACCAATGTGAATATTCATTAACCTGATGAGCTATTGAT 966
QY 1557 TACGGAACTCCGGGGACCACTGATGAACCTGATGCGAGGTCAATGGATCAACACG 1616
DB 967 TTTGAAACTCTGAGAGTCCCTGTGTTAACTGATGGGAGGTGATTTGAGTGAACACC 1026
QY 1617 CTCAAGTCAAGGCTGCGATCTCTTGGCATCCCTCCAGACCGCATCAACGCTTCTC 1676
DB 1027 ATGAAGTCAACAGCTGGAATCTCTTTCATCTTCTGATGTCTTCAAGATTTCTG 1086
QY 1677 ACAGAGTTCGAAGACACA-----GATCAAGACTGGAAGAGCGCTTCAATC 1724
DB 1087 CATCGTGGGGAAGAAAGAAATTCCTCTCCGAATCAATGGGTCCACGCGGCTACANT 1146
QY 1725 GGCATACGATGCGGACATCAACCAAGCTGTGATGACTGAAGCGCAGCAACCGG 1784
DB 1147 GGGGTGATGATGCTGACCTGATCCAGCATCTCTGTAATCAGCTTGAAGAACCA 1206
QY 1785 GACTCCGAGAGTCAAGAGTGAATTTATGCAAGAGTTGGCCGAAATTCACCTTCT 1844
DB 1207 AGCTTCCGAGTGTCAAGATGTGTACTCATCAATTAAGTATCTGGGCTCCCTGTGA 1266
QY 1845 CAGAGAGCGGATCCAGATGTGTGATCATCTGCAAGTCAACGCGCTCTCTAGTG 1904
DB 1267 CACCGGCTGTGTCTCGGCTGTGTATGATTTTGGCATTTGGGAGCAGATGATCA 1326
QY 1905 GACTGAGTGAAGTGTGAGAGGCGCTGTGAACGAGTCTCTCTTCTCTAGTGTGCGG 1964
DB 1327 AATGCTGAAGATGTTATGAAGCTGTTCGAACCAATCCAGTGTGGCAGTGAGATCCGG 1386
QY 1965 CGGGGGAACGACAGCTCTCTTCAGCATCGACCTGAGGT 2005
DB 1387 CGGGGAGCAAGAACACTGACCTTATATGTGACCTCTGAGGT 1427

RESULT 6
US-10-750-185-32084
Sequence 32084, Application US/10750185
Publication No. US200502603A1
GENERAL INFORMATION:
APPLICANT: NMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: NM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922

Query Match	4.3%	Score 130.2	DB 8	Length 908
Best Local Similarity	78.4%	Prid. No. 4.e-21		
Matches 156	Conservative	0	Mismatches 43	Indels 0
				Gaps 0
QY	1358	CAAGAAAAGCTCCCTGTGTTGTTGCTGGGTCACTGAGCCGACCTTGCGGACTT	1417	
Db	431	CCAGGAAAGCTGCTGTGCTACTGTGGCCGCTCTCGAGCTGGCGCCGGAGACTT	490	
QY	1418	TGTGTGGCCATTCGGCACTCCCTTCGCCCTACAGAAACACAGTACACACGGGATCGTGC	1477	
Db	491	CGTGTGCCCAATTGGAAGCCCGTITTCCTTCAAAACACGGTACACACGGGGATCGTCAG	550	
QY	1478	CACATCCACAGCGGAGGAGGACGAGAGCTGGGCTTCGGGACTCCGACATGGAATCAATCCA	1533	
Db	551	CACCAACCAAGGTGGTGGCAAAAGAACTGGGGCTCCGGAACTCGAGACTGACTATCA	610	
QY	1538	GACGATCCCATCATCAAC	1556	
Db	611	GAACAGACGCATCATCAAC	629	

Query Match	2.7%	Score 81.6;	DB 8;	Length 1497;
Best Local Similarity	52.8%	Pred. No. 1.6e-09;		
Matches 230; Conservative	0;	Mismatches 194;	Indels 12;	Gaps 2;

Oy 1182 GGCCTTCATCATGTGACAGAGCCGGCCTGAATCATATCAACAAATGCCAGCGTGGATGTCAGAGAAC 1241
 |||||
 Db 364 GGAATTGAACCTTGCGATTGCGGGCTTCATCATCATGACCAAAAAGCGCTACATCTGACCAATATACC 423
 |||||
 Oy 1242 AAGTCTGCCCCGGGGCAGCAGCAAGCTCAAGGTGACGTACAGAAATGGGAACTCTTAATGAG 1301
 |||||
 Db 424 CACGTGCTTCCCGGTATGGGAGAGTTCAAAAGTCTGTCTCAACGACAAAGCGGAATATATACC 483
 |||||
 Oy 1302 GCCCACCATTCAAAAGCATGTGACAAAGAAATGTGGACATTTGGCAACCATCAATCATCATCCCAAG 1361
 |||||
 Db 484 GCCAAACTCATCGGTTTCGATGTTCAAATCCGATGTGCGCTTCTGAAAATGACGCAACAG 543
 |||||
 Oy 1362 AAAAAGCTCCGTCGTGTTGTGTCGGGTCACTCGGCCGACTTCGCGGCTTGGGGAGTTGTG 1421
 |||||
 Db 544 GAAGAGGTACCCGTCCTCGTCAAAATCGGCATTCGCAAAAATTTGAACCGGGCGAAATGGGTTC 603
 |||||
 Oy 1422 GTGGCCATCGGCAAGTCCCTTTCGCTTACAGAAACAAGTACACAAACGGGAGATGCTGACACT 1481
 |||||
 Db 604 GCTGCGATTCGGCGCGGCTTCGCTTGTGACAAACAGGTATACCGCGGCATTCGTATCCG- 662
 |||||
 Oy 1482 GCCCAGCGGGAGGGCAGGAGCTTGAGCTTCGCGGAACTCCGACATGTGACTACATCCAGACG 1541
 |||||
 Db 663 -----CAAGGCAAGAGCTG---CCCAACGAAGGTACACACCTTTCATCCCAACC 711
 |||||
 Oy 1542 GATGCACTCATCACTAATAAGGAACTCCGCGGGGACCACTGTGTAAACCTGGATGCGGAGTTC 1601
 |||||
 Db 712 GACGTGTGCATCAATCCGGGCAAAATTCGCGGGCGCCGCTGTTCACATTAAAGGACAGGTTC 771
 |||||
 Oy 1602 AATTGGCATCAACAGGC 1617
 |||||
 Db 772 GTCCGCATCAATTGCG 787

RESULT 9
US-10-454-437-55
; Sequence 55, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompeju, Markus
; APPLICANT: Krogner, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zeller, Oskar
; APPLICANT: Haberneth, Gregor

;; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
;; FILE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
;; FILE REFERENCE: BGI-1280PCN
;; CURRENT APPLICATION NUMBER: US/10/454,437
;; PRIOR FILING DATE: 2003-06-13
;; PRIOR APPLICATION NUMBER: US 60/441031
;; PRIOR FILING DATE: 1999-06-25
;; PRIOR APPLICATION NUMBER: DE 19931636.8
;; PRIOR FILING DATE: 1999-07-08
;; PRIOR APPLICATION NUMBER: DE 19932125.6
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: DE 19932126.4
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: DE 19932127.2
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: DE 19932128.0
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: DE 19932129.9
;; PRIOR FILING DATE: 1999-07-19
;; PRIOR APPLICATION NUMBER: DE 19932226.0
;; PRIOR FILING DATE: 1999-07-09
;; PRIOR APPLICATION NUMBER: DE 19932920.6
;; PRIOR FILING DATE: 1999-07-14
;; PRIOR APPLICATION NUMBER: DE 19932922.2
;; PRIOR FILING DATE: 1999-07-14
;; Remaining prior Application data removed - See file Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 442
;; SEQ ID NO 55
;; LENGTH: 1446
;; TYPE: DNA
;; ORGANISM: Corynebacterium glutamicum
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (101)..(1423)
;; OTHER INFORMATION: RXA02630
US-10-454-437-55

Query Match
Best Local Similarity 2.2%; Score 66.2; DB 8; Length 1446;
Matches 168; Conservative 0; Mismatches 143; Indels 6; Gaps 1;

QY 1330 CGGACATGGCCACATCAAGATCCATCCCAAGAAAGCTCCCTGTGTGTGCTGGTGC 1389
DB 747 CAGATATTGCTGTGATCAAGATTAGGAGTGTCCCACTTCAGTTAGAGCTTTGGAG 806
QY 1330 ACTGGCGGACCTGGGGCTGGGGAGTTGTGTGCTGCGCATGCGCAGTCCCTTGGCCCTAC 1449
DB 807 ATTCGAGCGCATTAAGCGCTTGGCAAAAGTGTGATGCTGTGTCTTCCACTGGGCTGA 866
QY 1450 AGAACAAGTGAACAAGCGGATCTGACGATGCCCAAGCGGAGGCGAGGAG-----C 1503
DB 867 GCTCACTGTGACACACCGGATATGTGTGCGCGGTGAACCGTCTGTGGAGCTTCTGAGT 926
QY 1504 TGGGCTCCCGGAGCTCCGACATGAGCTACATCCAGAGCGATCCATCATCACTAAGGGA 1563
DB 927 ATGGGAGAGAGTGTCTCTCATGATGCTATCCAGACCAATCTGTGATCAACCTCGGTA 986
QY 1564 ACTCCGGGGGACCACTGCTGAACTGTGATGCGAGGCTCATTTGACATCAACAGCTCAAG 1623
DB 987 ACTGTGAGTGTGCGGTGCTGATGATGATGAGCAACCTCATTTGGCATGATGCTGTAATTG 1046
QY 1624 TCACGGGCTGCGCATTC 1640
DB 1047 CATCATTTGAGACACC 1063

RESULT 10
US-10-750-185-32073/c
; Sequence 32073, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.

;; APPLICANT: KERR, Richard
;; APPLICANT: ROSENFELD, David
;; APPLICANT: HOLM, Tom
;; APPLICANT: BATES, Stephen
;; APPLICANT: FANTIN, Dennis
;; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;; FILE REFERENCE: MM1100-2
;; CURRENT APPLICATION NUMBER: US/10/750,185
;; PRIOR FILING DATE: 2003-12-31
;; PRIOR APPLICATION NUMBER: US 60/437,482
;; PRIOR FILING DATE: 2002-12-31
;; NUMBER OF SEQ ID NOS: 64922
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 32073
;; LENGTH: 1376
;; TYPE: DNA
;; ORGANISM: Bovine 19866881129851
US-10-750-185-32073

Query Match
Best Local Similarity 2.1%; Score 62; DB 8; Length 1376;
Matches 83; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1587 CTGATGGCGAGGTGATTTGGCATCAACAGCTCAAGTCAAGCTGCGATCTCTTGGC 1646
DB 1214 CAGATGTGTAAGTATTTGAATTAAACACTGAAGGAGCAGCTGGAATCTCTTTGCA 1155
QY 1647 ATCCCTCAGACCGCATCAACAGGTTCTCTACAGAGTTCCAGACAGCATCAAG 1704
DB 1154 ATTCATCTGATTAAGATTAAAGTTCTCTTAACGGAATCCATGACCGAACCAAG 1097

RESULT 11
US-10-750-623-32073/c
; Sequence 32073, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32073
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Bovine 19866881129851
US-10-750-623-32073

Query Match
Best Local Similarity 2.1%; Score 62; DB 8; Length 1376;
Matches 83; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1587 CTGATGGCGAGGTGATTTGGCATCAACAGCTCAAGTCAAGCTGCGATCTCTTGGC 1646
DB 1214 CAGATGTGTAAGTATTTGAATTAAACACTGAAGGAGCAGCTGGAATCTCTTTGCA 1155
QY 1647 ATCCCTCAGACCGCATCAACAGGTTCTCTACAGAGTTCCAGACAGCATCAAG 1704
DB 1154 ATTCATCTGATTAAGATTAAAGTTCTCTTAACGGAATCCATGACCGAACCAAG 1097

RESULT 12
US-09-925-065A-873761

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/ Sequence 873761, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 873761
/ LENGTH: 577
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-925-065A-873761
```

```
Query Match 1.9%; Score 56.2; DB 6; Length 577;
Best Local Similarity 65.6%; Pred. No. 0.0013; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 43;
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```
QY 55 GGGCATATTCAGTCCATTTTTCAGATGAGGTTGAGGCCCCAGAGAAGTAACTTCT 114
DB 376 GGCTGTAGTATTCCTCATTTTACGAGAGGGTTGAGGCCAGAGAGGGGAGAGTT 435
QY 115 GTCTAGAGGCACACAGCTAGAAAGCAGCCAGCCCGGAGTGTGTGACGCC 174
DB 436 GGCTGAGGCACACAGCAGCCAGAGCCAGCCCTATCAATCTCCACCCCGTGCACCT 495
QY 175 CCCAG 179
DB 496 CTCAG 500
```

RESULT 13
US-10-750-185-32074/C
/ Sequence 32074, Application US/10750185
/ Publication No. US20050260603A1

```
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FATTIN, Dennis
/ TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-2
/ CURRENT APPLICATION NUMBER: US/10/750,185
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 32074
/ LENGTH: 1102
/ TYPE: DNA
/ ORGANISM: Bovine 19866881143159
US-10-750-185-32074
```

```
Query Match 1.8%; Score 54.8; DB 8; Length 1102;
Best Local Similarity 72.4%; Pred. No. 0.0033;
Matches 71; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
```

```
QY 1037 AGGTCTCCACGAGTCAGCAGCCCGCTACAACTTCACTTCTGACGTGTGA 1096
DB 289 AGGTGAGAGATCCCAACAGTCTGCGCATTAATACCTTTATTCGATGTGTGA 230
QY 1097 GAAGATCCGACGAGCGGTGTCCATAGAGCTCTTCC 1134
DB 229 GAAGATGCTCTGCGGTGTTCATCATGAACTGTTC 192
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RESULT 14
US-10-750-623-32074/C
/ Sequence 32074, Application US/10750623
/ Publication No. US2005028751A1

```
/ GENERAL INFORMATION:
/ APPLICANT: MMI GENOMICS, INC.
/ APPLICANT: DENISE, Sue K.
/ APPLICANT: KERR, Richard
/ APPLICANT: ROSENFELD, David
/ APPLICANT: HOLM, Tom
/ APPLICANT: BATES, Stephen
/ APPLICANT: FATTIN, Dennis
/ TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
/ FILE REFERENCE: MM1100-1
/ CURRENT APPLICATION NUMBER: US/10/750,623
/ CURRENT FILING DATE: 2003-12-31
/ PRIOR APPLICATION NUMBER: US 60/437,482
/ PRIOR FILING DATE: 2002-12-31
/ NUMBER OF SEQ ID NOS: 64922
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 32074
/ LENGTH: 1102
/ TYPE: DNA
/ ORGANISM: Bovine 19866881143159
US-10-750-623-32074
```

```
Query Match 1.8%; Score 54.8; DB 8; Length 1102;
Best Local Similarity 72.4%; Pred. No. 0.0033;
Matches 71; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
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```
QY 1037 AGGTCTCCACGAGTCAGCAGCCCGCTACAACTTCACTTCTGACGTGTGA 1096
DB 289 AGGTGAGAGATCCCAACAGTCTGCGCATTAATACCTTTATTCGATGTGTGA 230
QY 1097 GAAGATCCGACGAGCGGTGTCCATAGAGCTCTTCC 1134
DB 229 GAAGATGCTCTGCGGTGTTCATCATGAACTGTTC 192
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RESULT 15
US-09-925-065A-873523
/ Sequence 873523, Application US/09925065A
/ Publication No. US20040181048A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 873523
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LENGTH: 586
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-873523

Query Match 1.8%; Score 53.4; DB 6; Length 586;
Best Local Similarity 72.6%; Pred. No. 0.0061;
Matches 69; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Oy	55	GGGCAATTCA	GTCCCA	TTTTTCA	GATAGAG	AGTTGAG	GGCCCA	GAGAA	GTAA	GTATCT	114
Db	375	GGCTGTAGT	ATATCC	CAATTTT	ACAGAGAG	GGGTTG	AGGCC	CCAGAG	GGGCAG	GAAGTT	434
Oy	115	GTCTGAG	CCACAC	AGCTAG	AAAGCA	CCAGGCC	149				
Db	435	GCCTGA	AGCCAC	ACAGAG	CCCA	GAGGCC	CAGGCC	469			

Search completed: February 21, 2006, 19:51:53
Job time : 809 secs

c

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GenCore version 5.1.7
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OM nucleic - protein search, **Using FASTA model**

Run on: February 21, 2006, 19:58:21 ; Search time 17.9 Seconds

(without alignments)
2776.794 Million cell updates/sec

Title: US-10-617-443B-1

Perfect score: 5578
Sequence: 1 caggagactcgaagtttcag.....gcccaaaaaaaaaaaaaa 3006

Scoring table:

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Issued_Patents_AA -OPMT=fasten -SUFFIX=n2p.rat -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=humand4.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_AA:*
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2: /cgn2_6/prodata/1/1aa/6 COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/9 COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1060.5	19.0	480	2	US-09-949-016-6270 Sequence 6270, Ap
2	1053.5	18.9	480	2	US-08-923-454A-18 Sequence 18, Appl
3	1043.5	18.7	447	2	US-10-104-047-2765 Sequence 2765, Ap
4	1034.5	18.5	323	2	US-09-949-016-10514 Sequence 10514, A
5	906	16.2	458	2	US-08-923-454A-8 Sequence 8, Appl
6	903.5	16.2	458	2	US-08-923-454A-25 Sequence 25, Appl
7	903.5	16.2	458	2	US-09-008-271A-11 Sequence 11, Appl
8	903.5	16.2	458	2	US-09-968-415-11 Sequence 11, Appl
9	903.5	16.2	529	2	US-09-075-460-5 Sequence 5, Appl
10	900.5	16.1	458	2	US-08-923-454A-31 Sequence 31, Appl
11	878.5	15.7	400	2	US-09-724-864-55 Sequence 55, Appl
12	800.5	14.4	423	2	US-08-923-454A-6 Sequence 6, Appl

13	800.5	14.4	436	2	US-08-923-454A-29 Sequence 29, Appl
14	585.5	10.5	377	2	US-08-923-454A-27 Sequence 27, Appl
15	578	10.4	323	2	US-08-923-454A-4 Sequence 4, Appl
16	484	8.7	491	2	US-09-438-185A-980 Sequence 980, Appl
17	461	8.3	474	2	US-09-489-039A-13694 Sequence 13694, A
18	449.5	8.1	455	2	US-09-711-164-416 Sequence 416, Appl
19	448.5	8.0	355	2	US-09-711-164-417 Sequence 417, Appl
20	446	8.0	475	2	US-09-252-991A-29494 Sequence 29494, A
21	445	8.0	460	2	US-09-199-637A-132 Sequence 132, Appl
22	437.5	7.8	430	2	US-09-902-540-13405 Sequence 13405, A
23	432.5	7.8	499	2	US-09-673-898-6 Sequence 6, Appl
24	431	7.7	499	2	US-09-673-898-4 Sequence 4, Appl
25	429	7.7	499	2	US-09-673-898-2 Sequence 2, Appl
26	426.5	7.6	475	1	US-08-350-741-2 Sequence 2, Appl
27	426.5	7.6	475	1	US-08-463-878A-2 Sequence 2, Appl
28	426.5	7.6	477	2	US-09-543-681A-6204 Sequence 6204, Ap
29	425.5	7.6	541	2	US-08-311-731A-171 Sequence 171, Appl
30	425	7.6	474	2	US-09-689-065B-7 Sequence 7, Appl
31	424	7.6	173	2	US-08-923-454A-2 Sequence 2, Appl
32	424	7.6	414	2	US-09-388-090-6 Sequence 6, Appl
33	424	7.6	465	2	US-09-388-090-4 Sequence 4, Appl
34	423.5	7.6	409	2	US-09-902-540-11885 Sequence 11885, A
35	422.5	7.6	475	1	US-08-278-091-6 Sequence 6, Appl
36	422.5	7.6	475	1	US-08-483-859-6 Sequence 6, Appl
37	422.5	7.6	475	1	US-08-472-173-6 Sequence 6, Appl
38	422.5	7.6	475	1	US-08-487-167-6 Sequence 6, Appl
39	422.5	7.6	475	1	US-08-482-816-6 Sequence 6, Appl
40	422.5	7.6	475	1	US-08-296-149-6 Sequence 6, Appl
41	422.5	7.6	475	1	US-08-801-499-6 Sequence 6, Appl
42	422.5	7.6	475	1	US-08-615-271-6 Sequence 6, Appl
43	422.5	7.6	475	2	US-09-074-660-6 Sequence 6, Appl
44	422.5	7.6	475	2	US-09-074-660-6 Sequence 6, Appl
45	422.5	7.6	475	2	US-09-106-468-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-6270
Sequence 6270, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6270
LENGTH: 480
TYPE: PRT
ORGANISM: Human
US-09-949-016-6270
Alignment Scores:
Pred. No.: 2,066-72 Length: 480
Score: 1060.50 Matches: 241
Percent Similarity: 63.5% Conservative: 69
Best Local Similarity: 49.4% Mismatches: 117
Query Match: 19.0% Gaps: 61
DB: 12
US-10-617-443B-1 (1-3006) x US-09-949-016-6270 (1-480)
558 CCCCGCTGACACTGCTGTAGCCGAGGCTCGAGGAGACCACTGAGCCATGAGG 617
QY

Db	48	ProGlnProGlnHisCysGluGluGlyAlaGlyAlaAsp-----	60
Qy	618	AGAGGGCCAGTTCCTCTCTGAAGGGATTATGCTGATGAGGGAACAGACAGGCCCA	677
Db	61	-----AlaCys---GlyCysCysGluValCysGlyAlaProGluGlyAla	74
Qy	678	GGG---GGACTAACCCGAGATCCAGGCCCGGCTCACTCCGTGGCTCACGGCAATAT	734
Db	75	AlaCysGlyLeuGlnGluGlyProCysGlyGlyGlyGlnGlnCys-----	89
Qy	735	CCTAACCTCTCTGAGCCTCGGCCGACGCTTAGAGGGGTCCAGTGAAGGGGGGTAGGA	794
Db	90	-----ValValPro-----PheGlyValProAlaSerAlaThrVal	101
Qy	795	GCCGAGCAGCTGGAAGCCTTTTATACATCTTCGGGGTAGGAGAGCCCTTCCAAATGC	854
Db	102	ArgAlaGlyAlaGlnAlaGlyLeuGlyCysValCysAlaSerSerGluProVal-----	118
Qy	855	CTGGTGTCACTGCACTGCTGTGTGTGTAGGGGGTCCCAACGGGCTCACTGAGGGCTGAG	914
Db	119	-----CysGlySerAspAlaAsnThrTyAlaAsnLeuGlySerGlnLeuArg	133
Qy	915	CTGGCTCTGAACTGGGAGCAGGGGGTCTCAGGAAGAGCTCTCTCTGCGCCACTGGCAT	974
Db	134	AlaAla-----SerAlaGlySerGluArgLeu-----His	143
Qy	975	AGGCGCTCTGGAGCTGGCAGCATCTGTGATCTTCACTAGATGACACTGGACCTTCCGCCAGC	1034
Db	144	ArgPro-----ProValIleValLeuGlnArgGlyAla-----CysGly	156
Qy	1035	GCAAGTCTCCACCACTGAGCAGACGCCCGGCTCAAGATTCATCACTTATCTTGACGTGTG	1094
Db	157	GlnGlyGlnGluAspProAsnSerLeuArgHisGlyTyAsnPheIleAlaAspValVal	176
Qy	1095	GAGAAAGATGCGACCAAGCCGTGTCCACATAGAGCTCTTCTTGAGACACCCGCTTTTGGC	1155
Db	177	GluTyValIleAlaProAlaValAlaHisIleGluLeuPheArgGlyValLeuProPheSerLys	196
Qy	1155	CGCAACGTGGCCCTCTCCAGCGGTTCTGGCTTCATCATGTCCAGAGGGCGGCTGATCATCC	1214
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Qy	1215	ACCAATGCCCACTGTGTGTCCAGCAACAGTGTGCCCCGGGAGCAGCACTCAAGGTG	1274
Db	217	ThrAsnAlaHisValValThrAsn-----LysHisArgValLeuVal	230
Qy	1275	CAGCTACAGAAATGGGAGCTCCCTATAGGCGCCACATCAAGACATGCAAGAAATCGGAC	1333
Db	231	GluLeuLysAsnGlyAlaThrTyGlnAlaLysIleLysAspValAspGluLysValAsp	250
Qy	1335	ATTGGCAACATCAAAATCCATCCCAAGAAAAGCTCCGTGTGTCTTGCTGGGTCACTCG	1394
Db	251	IleAlaLeuIleLysIleAspHisGlnGlyLysLeuProValLeuLeuLeuGlyArgSer	270
Qy	1395	GCCGACCTGCGGGCTGGGAGATTGTGTGGTGGCCATCGCAGATCCCTTGCGCCTTACAGAC	1454
Db	271	SerGluLeuArgProGlyGluPheValValAlaIleGlySerProPheSerLeuGlnAsn	290
Qy	1455	ACAGTGAACAAGGGGATGTCAAGCACTGCCAGCGGGAGGGCAGGGAAGCTGGGCTCCGG	1514
Db	291	ThrValIleThrGlyIleValSerThrArgIleArgGlyGlyLysGluLeuGlyLeuArg	310
Qy	1515	GACTCCGACATGAGATTACATCCAGACGGATGGCATCACTACAGGGAACCTCGGGGGA	1574
Db	311	AsnSerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyLys	330
Qy	1575	CCACTGTGAACCTTGATGGCGAGGTCAATTGGCATCAACAGCTCAAGGTCAAGGCTGC	1634
Db	331	ProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAlaGly	350
Qy	1635	ATCTCTTTGCCATCCCTCAGACCGCATCACGGTCTTCACAGAGTTCCAAAGACAG	1694

Dd	351	IleSerPheAlaIleProSerAspLysIleLeuYbSpHeLeuThrGluSerHisAspArg	370
Gy	1695	CAGATCAAGAAC-----TGGAAGAAAGCGCTTCATCCGCATACGATGCCGCGATC	1741
Dd	371	GlnIleAlaYbGlyYbAlaIleThrIleYbYbLysTrileGlyIleArgMetCserLeu	390
Gy	1746	ACACCAGCCGTGTGGATGATGAGTGAAGCCACGACAACCGACTTTCCAGAGSTCKAGCACT	1801
Dd	391	ThreSeryLysAlaYbGluLeuYbAspArgHisAArgAspPheProAspValIleSer	410
Gy	1806	GGATTATTATGTCGAAGAGTGTCGCGCGAATTCACCTTCCAGAGAGGGGGCATCCAAAGT	1861
Dd	411	GlyAlaTryleIleGluValIleProaspThrProAlaGluAlaGlyIleuYbGlu	430
Gy	1866	GGTACATCATCTGTCAAAGTCAACGGCGAGTCCCTCATGAGCATCGAGTGCAGAG	1921
Dd	431	AsnAspValIleIleSerIleAsnGlyIneValValSerAlaAsnAspValSerAsp	450
Gy	1926	GCCGTGTGACCGAGTCTCTCTCTCATCTGAGAGTGGCGGGGGAACGACGACTCTCT	1986
Dd	451	ValIleYbAspGluSerThrLeuAsnMetValValAArgArgGlyAsnGluAsnIleMet	470
Gy	1986	TTCAGCATCGCACCTGAGAGTGGTC	2009
Dd	471	IleThrValIleProGluGluIle	478

RESULT 2

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US-08-923-454A-18
: Sequence 18, Application US/08923454A
: Patent No. 6004794
: GENERAL INFORMATION:
: APPLICANT: Creasy, Caretha
: APPLICANT: Livi, George
: APPLICANT: Karran, Eric
: APPLICANT: Clinkenbeard, Helen
: APPLICANT: Browne, Michael
: APPLICANT: Southan, Christopher
: TITLE OF INVENTION: HUMAN SERINE PROTEASE
: NUMBER OF SEQUENCES: 40
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Smithline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/923,454A
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/025436
: FILING DATE: 06-SEP-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Baumeister, Kirk
: REGISTRATION NUMBER: 33,833
: REFERENCE/DOCKET NUMBER: P50547
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 610-270-5096
: TELEFAX: 610-270-5090
: TELETYPE:
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 480 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide

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; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORIGINAL SOURCE: Feature - 213 gly/val polymorph
US-08-923-454A-18

Alignment Scores:
Pred. No.: 7,03e-72 Length: 480
Score: 1053.50 Matches: 240
Percent Similarity: 63.34 Conservative: 69
Best Local Similarity: 49.24 Mismatches: 118
Query Match: 18.94 Indels: 61
DB: 2 Gaps: 12

US-10-617-443B-1 (1-3006) x US-08-923-454A-18 (1-480)
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QY 678 GGG---GGACTAACCCAGATCCAGCCCGGCTCACTCCGCTGCTCAGCGCAATAT 734
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DB 90 -----ValAlaPro-----PheGlyValProAlaSerAlaThrVal 101
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DB 102 ArgArgArgAlaGlnAlaGlyLeuCysValCysAlaSerSerGluProVal----- 118
QY 855 CTGGGTCACTGCACTGCTGTGTGTGGGGGTCCCAAGCGGCTCAAGTGTGGCTGAGG 914
DB 119 -----CysGlySerAspAlaAsnThrTyAlaAsnLeuCyseGlnLeuArg 133
QY 915 CTGGCTGTGAATGAGGAGGAGGCTCTCAGGAAGAGGCTCTCTGCTGCGCACTGGGCA 974
DB 134 AlaAla-----SerArgArgSerGluArgLeu-----His 143
QY 975 AGGCTCTGGAGCTGGCAGCATCTGATCTCAATGATGCACTGGCCCTTCCCGCAGC 1034
DB 144 ArgPro-----ProValIleValLeuGlnArgGlyAla-----CysGly 156
QY 1035 GCAAGTCTTCACAGCTGACGACCCCGGCTCAAGATTCACTTCACTTCTGAGCTGTG 1094
DB 157 GlnGlyGlnGluAspProAsnSerLeuArgHisIleTyAsnPheIleAlaAspValVal 176
QY 1095 GAGAAGATGACACAGCGGTGTCCACATAGAGCTCTTCTGTAGACACCGCGTGTGGC 1154
DB 177 GlnLeuValIleAlaProAlaValAlaIleGlnLeuPheArgGlyLeuProPheSerIle 196
QY 1155 CGCAAGCTGCGCCCTGTCAGACCGGTTCTGCTTCACTATGCTCAGAGGCGCGCTGATC 1214
DB 197 ArgGluValProValAlaSerGlySerGlyPheIleValSerGluAsp**LeuIleVal 216
QY 1215 ACCAATGCCACAGTGTGTCTCAGCAAGCTGCTGCCCGGCGACGACGACGCTCAAGTG 1274
DB 217 ThrAsnAlaHisValValAlaThrAsn-----LysHisArgValIleVal 230
QY 1275 CAGCTACGAATGGGAGCTCTATGAGCGCACATCAAGACATCAAGAAAGTCGAGC 1334
DB 231 GlnLeuValSerGlyAlaThrTyArgIleValIleValIleValAspValAspGluValAsp 250
QY 1335 ATGGCACCATCAAGATCCATCCCAAGAAAGCTCTCTGCTGTGTGCTGGGCTGAGC 1394
DB 251 IleAlaLeuIleIleValIleAspHisGlnGlyLeuPheProValIleLeuLeuGlnArgSer 270

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QY 1395 GCCGACCTGCGGCGCTGGGAGGTTGTGTGGTCATCGGACGCTTGCCTTACAGAAC 1454
DB 271 SerGlnLeuArgProGlnValPheValAlaIleGlySerProPheSerLeuGlnHis 290
QY 1455 ACAGTCAACAGCGGCTGTGACGACTGCGCAGCGGAGGAGGAGGAGCTGGGCTCCGG 1514
DB 291 ThrValThrThrGlnIleValSerThrThrGlnArgGlyGlyLeuGlnLeuGlyLeuArg 310
QY 1515 GACTCCGACATGAGCTATCATTCACAGCGATCCATCATCATCACTACGGAACTCCGGGGA 1574
DB 311 AsnSerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyGlyAsnSerIleGly 330
QY 1575 CCAGTGGAGAACTGAGAGGCGAGGCTGATGTCATCAACAGCTCAAGTCAAGCTGAGC 1634
DB 331 ProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuValThrAlaGly 350
QY 1635 ATCTCTTGTGCATCCCTCAGACCGCATCAACGCTTCTTCAAGAGTTCACAGAAC 1694
DB 351 IleSerPheAlaIleProSerAspTyrIleLeuValSerPheLeuThrGluSerHisAspArg 370
QY 1695 CAGATCAAAAGC-----TGAAAGAGCGCTTCACTCGCATACGATCGGACGATC 1745
DB 371 GlnAlaValGlyValAlaIleThrIleValSerTyrIleGlyIleArgMetSerLeu 390
QY 1746 ACACCAAGCTGTGATGAGCTGAGGCGCAAGCAACCGGACTTCCAGAGGTGACAGT 1805
DB 391 ThrSerSerLeuValAlaGlyLeuValAspArgHisAspAspPheProAlaIleSer 410
QY 1806 GGAATTATGTGCAAGAGTTGCGCGAATTCACCTTCTCAGAGAGGCGGCTCAAGAT 1865
DB 411 GlyAlaTyrlleIleGlnValIleProAspPheProAlaGlnAlaGlyGlyLeuValGlu 430
QY 1866 GGTGACATCATCTGACAGCTCAACGCGCTCTCTAGTGAAGCTCGAGTGAAGTGAAG 1925
DB 431 AsnAspValIleIleSerIleAsnGlyGlnSerValIleSerAlaAsnAspValSerAsp 450
QY 1926 GCCGTGACCGAGTCTCTCTCTCTGAGAGTGGCGGCGGAGGAGCAAGCACTCCG 1985
DB 451 ValIleValArgGluSerThrLeuAsnMetValValAlaArgGlyAlaGlnAspIleMet 470
QY 1986 TTCAGCATCGACCTGAGTGTGTC 2009
DB 471 IleThrValIleProGlnGluIle 478

RESULT 3
US-10-104-047-2765
; Sequence 2765, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2765
; LENGTH: 447
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-104-047-2765

Alignment Scores:
Pred. No.: 3.94e-71 Length: 447
Score: 1043.50 Matches: 241
Percent Similarity: 65.18 Conservative: 72
Best Local Similarity: 50.18 Mismatches: 97
Query Match: 18.78 Indels: 71
DB: 2 Gaps: 14

US-10-617-443B-1 (1-3006) x US-10-104-047-2765 (1-447)

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Db 22 ProAhrgrArgrSerProAlaLeuAlaLeuSerhenthThrYrAlaenLeuCySgInGln 41
QY 642 -----GGTATTCCTGTAGCATGAGGAGACAGCAAGAGCCGAGGGGACTPACCCAGAT 695
    ||||| ||||| ||||| |||||
Db 42 ArgAlaGlyValArgLeuLeuArgGlyValArgArgAlaArgValArgValArg--- 60
QY 696 CCAAGCCCCGCGCTACCCGCTGTGGCTCACGGGCAATTCCTAACTCTCTGTAGAGCTTC 755
    ||||| ||||| ||||| |||||
Db 61 ProAlaGlyValProValArgArgGlyAla-----AlaVal 72
QY 756 CTCGCCAGCTTAGAGGGCTCCAGTAGAGGGGGGTAGAGAGCCGAGCAGCTGAAAGCTT 815
    ||||| ||||| ||||| |||||
Db 73 ArgGlyValAlaLeuArgGlyAlaSerLeuGlyHisGlyValAlaAlaAlaArg----- 88
QY 816 TTAACCATTTCTCGGGGTAGCGAGAGCCCTTCCCAATGCTGTGTCTCATCTGCTGT 875
    ||||| ||||| ||||| |||||
Db 89 -----AlaGlyArgProLeu-----Cys 94
QY 876 GTGTAGAGGGGTCCCAAGGGGCTCAGTGTGGGTGAGGCTGGCTTGAATGGGACAG 935
    ||||| ||||| ||||| |||||
Db 95 Val-----ArgGlnGln-----LeuArgAlaAla----- 102
QY 936 GGTCTCAGAGAGAGCTCTCTCTCTGCGCCATGCGGATAGAGGCTGTGGAGCTGGCAG 995
    ||||| ||||| ||||| |||||
Db 103 ---SerAhrgrArgrSerGluArgLeu-----HisArgPro----- 112
QY 996 ATGTGATCTCATGTATGACCTGTGGCCCTTCCGCCAGCGAGCTTCACCAAGCTGAGC 1055
    ||||| ||||| ||||| |||||
Db 113 ProValIleValLeuGlnArgGlyAla-----CysGlyGlnGlyGlnArgProLeu 130
QY 1056 AGCCCGGCTACAGAGTTCACTCATGTGTGAGAGGTGTGAGAGAGTCCGACAGCCG 1115
    ||||| ||||| ||||| |||||
Db 131 SerLeuArgHisArgYrAanPheIleAlaAspValValGlnArgIleAlaProAlaVal 150
QY 1116 GTCCACATAGAGCTCTTCTCTGAGACACCCGCTGTTTGGCCGACAGCCCTGTGCAG 1175
    ||||| ||||| ||||| |||||
Db 151 ValHisIleGluLeuPheArgGlySerProPheSerArgGlyValProValAlaSer 170
QY 1176 GGTTCGTGGCTTCATGTCTAGAGGCGGCTGATATCATCAATGCCAGCTGGGTGTC 1235
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Db 171 GlySerGlyPheIleValSerGluAspGlyLeuIleValThrAsnAlaHisValValThr 190
QY 1236 AGCAACAGTGTCTCCCGGCGAGGACAGCTCAAGTGCATCAAGATGGGAGCTCC 1295
    ||||| ||||| ||||| |||||
Db 191 Asn-----LysHisArgValValGluValGluLeuLysAsnGlyAlaThr 204
QY 1296 TATGAGGCCACATCAAGACATCGACAGAGTGGGACATTGCCACATCAAGATTCAT 1355
    ||||| ||||| ||||| |||||
Db 205 TyrGluAlaIleArgIleValAspValAspGluValAlaAspIleAlaLeuIleValAsp 224
QY 1356 CCCAAGAAAAAGCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1415
    ||||| ||||| ||||| |||||
Db 225 HisGlnGlyValLeuProValIleLeuLeuGlyArgSerSerGluLeuArgProGlyGln 244
QY 1416 TTGTGTGTGGSCATTCGSCATCCCTTCCGCTTCAGAGACAGTGAACAAGGGGACATGTC 1475
    ||||| ||||| ||||| |||||
Db 245 PheValValAlaIleGlySerProPheSerLeuGlnAsnThrValThrArgIleVal 264
QY 1476 AGCACTGCCAGCGAGGAGGAGGAGCTGGGCTCCGAGCTCCGACATGACTCATATC 1535
    ||||| ||||| ||||| |||||
Db 265 SerThrThrGlnArgGlyGlyValGluLeuGlyLeuArgAsnSerAspMetArgYrIle 284
QY 1536 CAGACGGATGCCATCATCACTACGGGAATCTCCGGGGGACCACTGTGAACTGTAGTGGC 1595
    ||||| ||||| ||||| |||||
Db 285 GlnThrAspAlaIleIleAsnArgGlyAsnSerGlyGlyProLeuValAsnLeuAspGly 304
QY 1596 GAGTCATTGGCATCAACAGCTCAAGGTGACGGGCTGGCATTCCTTGGCATCCCTCA 1655
    ||||| ||||| ||||| |||||
Db 305 GluValIleGlyIleAsnThrLeuValThrAlaGlyIleSerPheAlaIleProSer 324
```

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QY 1656 GACCCGATCACAGGTTCTCTCACAGATTCCAAGACAAAGACATCAAGAC----- 1706
    ||||| ||||| ||||| |||||
Db 325 AspLysIleValPhePheLeuThrGluSerHisAspArgGlnAlaValGlyValAlaIle 344
QY 1707 TGAAGAGACGCTTCACTTCGCGATTCAGATGCGGACGATCAACCAAGCTGTGTGATGAG 1766
    ||||| ||||| ||||| |||||
Db 345 ThrLysValPheThrIleGlyIleArgMetSerLeuThrSerSerLysValLysGln 364
QY 1767 CTGAAGGCCAGACACCCGAGCTTCCAGAGGTCAGACAGTGAATTTATGTCAAGAGTT 1826
    ||||| ||||| ||||| |||||
Db 365 LeuLysAspArgHisArgAspPheProAspValIleSerGlyAlaThrIleIleGluVal 384
QY 1827 GCGCGAATTCACCTTCTCAGAGAGCGGCGATCAAGATGTGATCATCTGACATGATC 1886
    ||||| ||||| ||||| |||||
Db 385 IleProAspThrProAlaGluAlaGlyLeuArgGluAsnAspValIleIleSerIle 404
QY 1887 AACGGGCGTCTCTAGTGTGATGATCGAGTGTGAGAGGCGGTGTGACGAGTCTCT 1946
    ||||| ||||| ||||| |||||
Db 405 AsnGlyGlnSerValValSerAlaAsnAspValIleLysArgGluSerThr 424
QY 1947 CTCCTACTGAGAGTGGGCGGAGGAGACGACCTTCCTTACGATGCGACCTGAGGTG 2006
    ||||| ||||| ||||| |||||
Db 425 LeuAsnMetValValArgArgGlyAsnGluAspIleMetIleThrValIleProGluGln 444
QY 2007 GTC 2009
    ||||| ||||| ||||| |||||
Db 445 Ile 445

RESULT 4
US-09-949-016-10514
; Sequence 10514, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10514
; LENGTH: 323
; TYPE: PR
; ORGANISM: Human
US-09-949-016-10514

Alignment Scores:
Pred. No.: 1,65e-70 Length: 323
Score: 1034.50 Matches: 203
Percent Similarity: 80.4% Conservative: 60
Best Local Similarity: 62.1% Mismatches: 55
Query Match: 18.5% Indels: 9
DB: 2 Gaps: 2

US-10-617-443B-1 (1-3006) x US-09-949-016-10514 (1-323)
QY 1038 GGTCTCCACACAGCTAGAGCGCCGCGGACAAAGTTCAATTCATGTTGAGCTGGTGGAG 1097
    ||||| ||||| ||||| |||||
Db 1 GlyGlnGluAspProAsnSerLeuArgHisArgYrAanPheIleAlaAspValValGln 20
QY 1098 AAGATCGACCAACCGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1157
    ||||| ||||| ||||| |||||
Db 21 LysIleAlaProAlaValAlaHisIleGluLeuPheArgGlyLeuProPheSerLysArg 40
QY 1158 AACGTGCCCTGTCCAGCGGCTTGTGCTTCATCATGTCTAGAGGCGGCGCTGATCATCAC 1217
    ||||| ||||| ||||| |||||
```

```

STREET: 709 Swedeland Road
City: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-923-454A-8

Alignment Scores:
Pred. No.: 1,23e-60 Length: 458
Score: 906.00 Matches: 211
Percent Similarity: 62.8% Conservative: 90
Best Local Similarity: 44.1% Mismatches: 125
Query Match: 16.2% Indels: 53
DB: 2 Gaps: 11

US-10-617-443B-1 (1-3006) x US-08-923-454A-8 (1-458)

QY 620 AGGCGCAGTTCTCTCTGTGAAGGATATTGCTGTAGCATGAGGAAACAGACAAAGGCCACG 679
Db 15 ArgAlaIrrpArAlaArgAlaLeuGlyGlyIleCysIrrpGlyArGArg----- 28
QY 680 GGAGCTAACCCGGAATCCAGCCCGCGGCTCACTCCCGTGGGCTCAGCGCAATATCTCAA 739
Db 29 -----PrArGleuIrrPrArGleuArGAlaLeuIrrSer 41
QY 740 CCTCTCTGTAGCCTCTCTGCGCCAGCCTAGCAGGCTCCAGTCAAGAGGGGGGTGAGAAAGCCCA 799
Db 42 GlyIrrSerArSpPrArGAlaArGValIrrIrr-----GlyIrrPr 55
QY 800 GCACGTGAGAGCCTTTTAAACCATTTCTGGGGGTGAGCAGCAGCCCTTCCAAATGCTTGGT 859
Db 56 Ser-IrrIrrPrArIrrArGleuSerVal---GlyValIrrIrrIrrPro---ArGAlaCySerIrr 73
QY 860 GTCACTGCACACGTGTGTGTGTGTTAGGGGGGTCCC---CAAGGGGCTCAGTGTGGGCTAGAGCT 916
Db 73 rSer-----GlyIrrPrGlyPrArGAlaGleuIrr-----Irr 84
QY 917 GGCTCTGAACTGGGACAGGGGCTTCAGAGAGAGCCTCTCTCTGCCACTGGGCGATAG 976
Db 84 rAlaValIrrPrArSpIrrArGThrArGAlaIrrSerCylubSerGlyIrrArGSerAr 104
QY 977 G-----CCTCTGGAGAGCTGGCAGCATGCTGATCTCACTGATG----- 101

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Db      42 GlyThrSerProAlaArgValThrTyr-----GlyThrPro 55
QY      800 GCACGTGGAGCCTTTTAAACATTCTCGGGGTGAGGAGCCCTTCCCAATGCTGT 859
Db      56 SerLeuThrPalaArgLeuSerVal---GlyValThrGluPro---ArgAlaCysLeuTh 73
QY      860 GTACATGCACTGCTGTGTGTAAGGGGGTCC---CAACGGGCTCAGTGTGGGCTGAGGCT 916
Db      73 rSer-----GlyThrProGlyProAlaGluLeu-----Th 84
QY      917 GGCTGTGAACCTGGACAGGGGTCTCAGAGAGCCTCTCTCCCTGCCACATGCGGATAG 976
Db      84 rAlaValThrProAspThrArgThrArgGluAlaSerGluAsnSerGlyThrArgSerAr 104
QY      977 G-----CCTCTGGAGCTGGCAGCAGTCATGATCTCACTGATG----- 1013
Db      104 gAlaThrLeuAlaValAlaLeuGlyAlaGlyAlaValLeuLeuLeuThrGlyGly 124
QY      1014 -----CACCTGGCCTTCCCGCAGCGCAGCTCTCCACAGCTGACGACCGCGG 1063
Db      124 yGlyArgGlyProProAlaValLeuAlaAlaValProSerProProAlaSerProAr 144
QY      1064 CTCAAGTTCAACTTCATTGCTGACGTGTGAGAGAGATGCAACAGCCGTGTGTCACAT 1123
Db      144 gSerGlnTyrAsnPhenIleAlaAspValValGluValThrAlaProAlaValTyrI 164
QY      1124 AGAGCTCTTCTTGAGACACCCGCTGTTGGCCCGCAGACGTGCCCTGTCACGCGTTCG 1183
Db      164 eGluIleLeuAspArgHisProPheLeuGlyArgGluValProIleSerAsnGlySerG 184
QY      1184 CTTCATCATGTGCAAGGCGCGCTGATCACCACATGCCCAGGTGTGTCCAGCAACAG 1243
Db      184 yPheValValAlaAlaAspGlyLeuIleValIThrAsnAlaHisValAlaAsp----- 202
QY      1244 TGCTGCCCGCGGAGCAGCAGCTCAAGTGTGACCTAAGATGGGGACTCTATAGGC 1303
Db      203 -----ArgArgArgValAlaArgValArgLeuLeuSerGlyAspThrArgGluAl 218
QY      1304 CACCATCAAGAATGTCACAGAGATCGACATTCGCACATCAAGTCCATCCCAAGAA 1363
Db      218 aValValIThrAlaValAspProValAlaAspIleAlaThrLeuArgIleGlnThrArg 238
QY      1364 AAAGCTCCCTGTGTGTGCTGGGTCACTGCGCGCAGCTGCGGCTGGGGAGTTTGGT 1423
Db      238 uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyGluPheValVa 258
QY      1424 GGCCATCGGCAGTCCCTTCGCTTACAGAAACAGATGACACGGGATCTGTAGCACTGC 1483
Db      258 lAlaMetGlySerProPheAlaLeuGlnAsnThrIleThrSerGlyIleValSerSerAl 278
QY      1484 CCAAGCGGAGGAGGAGGAGCTGGGCTCCGGGACTCCGACATGAGTACATCCAGACGA 1543
Db      278 agIAspArgProAlaArgAspLeuGlyLeuProGlnThrAsnValGluTyrIleGlnThrAs 298
QY      1544 TGCCATCATCAATCAGCGGAATCCGGGGAGCACTGTGATGATGGATGGCAGGATCAT 1603
Db      298 pAlaAlaIleAspPheIleAspPheIleGlyProLeuValAlaAsnLeuAspGlyGluVal 318
QY      1604 TGCCATCAACACGCTCAAGGTCAAGGCTGGCATCTCTTGGCATCCCTCAGACCGCAT 1663
Db      318 eGlyValAsnThrMetLeuValThrIaGlyIleSerPheAlaIleProSerAspArgLe 338
QY      1664 CACACGGTTCCTCAGACAGTTCACAGACAGCAG-----ATCAAAATCTGGA 1711
Db      338 uArgGluPheLeuHisArgGlyGluTyrGlyAsnSerSerSerGlyIleSerGlySerG 358
QY      1712 GAAGCGTTATCATGCGCATGAGATGCGGAGATCAACCAAGCTGTGATGAGCTGAA 1771
Db      358 nArgArgGlyTyrIleGlyValMetLeuThrLeuSerProSerIleLeuAlaGluLeuG 378
QY      1772 GGCAGACCAACCGGACTTCCAGAGGTCAAGTGAATTATGTGCAGAGGTTGCGCC 1831

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Db      378 nLeuArgGluProSerPheProAspValGlnHisGlyValLeuIleHisLeuValIleLe 398
QY      1832 GAATTACCTTCTCAGAGAGCGGCGCATCCCAAGTGTGATCATCATCTGAAGTCAACG 1891
Db      398 uGlySerProAlaHisArgAlaGlyLeuArgProGlyAspValIleLeuAlaIleGlyG 418
QY      1892 GCGTCTCTAGTGAATCAGTGAAGTGAAGAGCGGCTGTGACAGTCTCTCTCT 1951
Db      418 uGlnMetValGlnAsnAlaGluAspValTyrGluAlaValArgThrGlnSerGlnLeuAl 438
QY      1952 ACTGAGGTGCGCGGGGAGACGACACCTCTTCAAGATCGACCTGAGGTG 2006
Db      438 aValGlnIleArgArgGlyArgGluThrLeuThrLeuTyrValThrProGluVal 456

RESULT 8
US-09-968-415-11
; Sequence 11, Application US/09968415
; Patent No. 6855811
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
; Tang, Tom Y.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,415
; FILING DATE: 26-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/659,151
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohan-Peterson, Sheela
; REGISTRATION NUMBER: 41,201
; REFERENCE/DOCKET NUMBER: PF-0458 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SINDUCT01
; CLONE: 2680548
; SEQUENCE DESCRIPTION: SEQ ID NO: 11 :
US-09-968-415-11

Alignment Scores:
Pred. No.: 1,9e-60 Length: 458
Score: 903.50 Matches: 208
Percent Similarity: 65.1% Conservative: 91
Best Local Similarity: 45.3% Mismatches: 116
Query Match: 16.2% Indels: 44
DB: 2 Gaps: 12

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QY 766 TAGCAGGGTCAGTGAAGGGGGTGAAGAACCCAGACGTTGAAGCCTTTTAACATTC 825
Db 55 -----ProserLeutrp--AlaaglySerVal- 63
QY 826 TCGGGGTGAGCAGCCCTTCCCAATGCTGGTGTCACTGCACTGCTGTGTGTAGGG 885
Db 64 --GlyValthrGluPro--ArgAlaCylLeuThrSer-----GlyT 76
QY 886 GTCCC---CAAGGGGTCTAGTGGGCTAGAGCTGGCTCTGAAGTGGACAGGGCTCA 942
Db 76 hrProGlyProArGAlaGlnLeu-----ThrAlaValThrProArGTrhArGTrhA 93
QY 943 GGAAGAGCTCCTCCCTCCGACCGGAGCATAGG-----CCTGGGGAG 987
Db 93 rGlnuAlaSerGluLeuSerGlyThrArGSerArGAlaTrpLeuAlaValAlaLeuGlyA 113
QY 988 CTGGCAGCATCGTGAATCTCATGTATG-----CACTGGCCCTTCCCG 1029
Db 113 laGlyGlyAlaValLeuLeuLeuLeuLeuTrpGlyGlyAlaGlyArGlyProProAlaValLeuA 133
QY 1030 CCAAGCCAGGTCTCCACAGCTGAGCAGCCCGGCTCAACAATTCAATTGCTGAGC 1089
Db 133 laAlaValProSerProProAlaSerProArGSerGlnTrhArhPheIleAlaAspV 153
QY 1090 TGGTGGAGAAGATCGCAGCAGCGGTGTCACATGAGCTCTTCCGAGACCCGCTGT 1149
Db 153 aValaGluTrhArhAlaProAlaValaValTrIleGluLeuSerhPheAlaProPheL 173
QY 1150 TTGGCCGCAACGTGCCCTGTGCAGCGGTCTGCTTCATGTCATGTCAGAGCGGCTGA 1209
Db 173 euGlyArGlnuAlaProIleSerArhGlySerGlyPheValaValAlaAlaAspGlyLeuI 193
QY 1210 TCATCAACCAATGCCCACTGTGTGTCCAGCAACAGTGTGCCCCGGGAGGACAGCACTCA 1269
Db 193 leValThrArhAlaIleAlaValaValaAlaAsp-----ArGArGArGVala 207
QY 1270 AGGTGACCTACAGATGGGGGACTCTTATAGGGCCACATCAAGAAGCATGCAAGAAGT 1329
Db 207 rGValaArgLeuLeuSerGlyAspTrhTrIyGlnuAlaValaValaValaAlaAspProVala 227
QY 1330 CGACATTTGCCACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTGTGTGCTGAGTC 1389
Db 227 laAspIleAlaThrLeuArGTrIleGlnTrhLeuGluProLeuProThrLeuProLeuGlyA 247
QY 1390 ACTCGGCCGACCTGCGGCTGCGGAGTTTGTGGTGCATCGGACGTCCCTTGGCCCTAC 1449
Db 247 rGSerAlaAspValaArgGlnGlyGluPheValaValaAlaMetGlySerProPheAlaLeuG 267
QY 1450 AAGAACAAGTGAACAAGGGGACCTGTCAGACATGCCAAGGGGAGGAGGAGGAGCTGGGC 1509
Db 267 laAsnThrIleThrSerGlyIleValaSerSer**GlnArGProAlaAspAspLeuGlyL 287
QY 1510 TCCGGGACTCCGACATGACTACATCCAGACGAGATGCCATCACTACAGGGAATCCG 1569
Db 287 eurProGlnTrhArhValaGlyTrIleGlnTrhArhAlaAlaIleAspPheGlyAsnSerG 307
QY 1570 GGGGACCACTGTGAACCTGATGGGAGGTCAATTGGATCAACACGCTCAAGTCAAGC 1629
Db 307 lyGlyProLeuValaLeuLeuAspGlyGluValaIleGlyValaAsnThrMetCylValaThrA 327
QY 1630 CTGGCATCTCTTGGCATCCCTTCCAGACCGCATCAACAGGTCTCCACAGAGTCCAG 1689
Db 327 laGlyIleSerPheAlaIleProSerAspArgLeuArGTruPheLeuAlaArGlyGluL 347
QY 1690 ACAAGCAG-----ATCAAGAAGTGAAGAGAGGCTTCATCGGATACGGATGC 1737
Db 347 yLylAsnSerSerSerGlyIleSerGlySerGlnArGArGTrylleGlyValaMetMetL 367
QY 1738 GGAACATCAACCAAGCTGTGGATGAGCTGAAGCCGCAACCCGGAAGTCCCAAGC 1797
Db 367 eufThrLeuSerProSerIleLeuAlaGluLeuGlnLeuArGTruProSerPheProAspV 387

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QY 1798 TCAGACGTGAATTATGTGCAGAGGTGCGCCGAATTCACCTTCTCAGAGGCGCA 1857
Db 387 alGlnIleGlyValLeuLeuIleHisLysValIleLeuGlySerProAlaHisArGAlaGlyL 407
QY 1858 TCCAAATGGTGAATCATCTCAAGGTCAAGGCGGCTCCCTAGTGAATCGAGTAC 1917
Db 407 euaArgProGlyAspValIleLeuAlaIleGlyGlnGlnMetValGlnAsnAlaGluAspV 427
QY 1918 TGCAGAGGCGCGTGTGCAGGAGTCTCCCTCTCTGAGAGGTGGCGGGGGAACAGC 1977
Db 427 alTrGlnuAlaValaArgTrhGlnSerGlnLeuAlaValaGlnIleArGArGlyArGTru 447
QY 1978 ACCTCTCTTCAATCGCACCTGAGTGTG 2006
Db 447 hrLeuThrLeuTrhValaThrProGluVal 456

RESULT 11
US-09-724-864-55
; Sequence 55, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 400
; TYPE: PRF
; ORGANISM: Mouse
US-09-724-864-55

Alignment Scores:
Pred. No.: 1,44e-58 Length: 400
Score: 878.50 Matches: 181
Percent Similarity: 68.0% Conservative: 63
Best Local Similarity: 50.4% Mismatches: 64
Query Match: 15.7% Indels: 52
Gaps: 4

US-10-617-443B-1 (1-3006) x US-09-724-864-55 (1-400)
QY 1069 AGTTCACCTTCAATGCTGACCGTGTGAGAGATGCGACCCAGCTGTGTCATAGAC 1128
Db 47 SerTrhTrhSerSerProGlnTrIyPrhArGArGTrpArGArGLeuTrpSerTrhCySer 66
QY 1129 TCTTCTG-----AGACAC----- 1142
Db 67 CysSerAlaAspAspArhGHisThrGlySerHisThrAspLeuLysGluGluThrProSer 86
QY 1142 ----- 1142
Db 87 TrpTrhGlnIleSerValaValaPheArGTruAspGlyGlnAspGluLeuGlnAlaAlaHis 106
QY 1143 -----CCGCTGTTTGGCCGCAAGTGCAGTCCCTGTCAGCGGTTCT 1181
Db 107 lyValaHisGlySerGlySerProLeuTrhArhGlnGlnIleProSerSerGlySer 126
QY 1182 GGGTTCATCATGTCAAGGCGGCTGATCATCAACATGCCACGTGTGTCCAGAAC 1241
Db 127 GlyPheIleValaSerGluAspGlyLeuIleValaThrAsnAlaHisValaLeuThrAsn--- 145
QY 1242 AGTGTGCGCCGCGGAGGACGAGACGCTCAAGTGTGACGTACAGAAAGGGGAGCTCCATGAG 1301
Db 146 -----GlnGlnLysAlleGlnLysAlaGluLeuGlnSerGlyAlaArGTruGlu 160
QY 1302 GCCACATCAAGAAGATGAGCAAGAAAGTGCAGCATTTGCCACATCAAGTCCATCCAG 1361

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Db      |||||.....||| |||..... |||||..... |||
161 AlAtNrValValAspIleAspHisIleValAspLeuAlaLeuIleValIleGluProAsp 180
QY      1362 AAAAAGCTCCCTGTTGTTGTTGCTGCTGAGCCGACCTGGCGGAGTTGG 1421
Db      .....|||..... |||..... |||..... |||
181 ThrGluLeuProValIleuLeuLeuGlyIAspSerSerAspLeuValIleGluProVal 200
QY      1422 GTGGCCATCGGAGAGTCCCTTCGCTTACAGAACACAGTGAACAACGGGACCTGTCAGACT 1481
Db      .....|||..... |||..... |||..... |||
201 ValAlaLeuGlySerProPheSerIleuGlnAsnThrValThrAlaGlyIleValSerThr 220
QY      1482 GCCCAGCGGAGGACGGAGAGCTGGGCTTCGGGAGTCCGACATCGACATCCAGAG 1541
Db      .....|||..... |||..... |||..... |||
221 ThrGluIAspGlyValArgGluLeuGlyLeuValAsnSerAspIleAspTyrIleGlnThr 240
QY      1542 GATGCATCATCAACTACCGGAACTCCGGGGACCACTGGTGAACCTGATGGCGAGTGC 1601
Db      .....|||..... |||..... |||..... |||
241 AspAlaIleIleAsnHisIleGlyAsnSerGlyValProLeuValAsnLeuAspGlyAspVal 260
QY      1602 ATTGCATCAACAACGCTCAAGGTCAACGCTGAGCTCTTGGCATCCCTCAAGACCG 1661
Db      .....|||..... |||..... |||..... |||
261 IleGlyIleAsnThrIleuValThrAlaGlyIleSerPheAlaIleProSerAspArg 280
QY      1662 ATCAACACGGTCTCTCAACAGATTCACAGACACAGACATCAAA-----GACTGGAG 1712
Db      .....|||..... |||..... |||..... |||
281 IleArgGluPheLeuGluIleAspTyrHisGluArgGluLeuGlyValAspLeuGln 300
QY      1713 AAGCGCTCATCGGCTACGATGCGGATGCGGACATCAACAACGCTGGTGAATGAGTGAAG 1772
Db      .....|||..... |||..... |||..... |||
301 LysValTyrIleuGlyLeuAspMetLeuProLeuThrLeuAsnLeuGlnGluMetLys 320
QY      1773 GCCAGAACCCGAGCTTCCAGAGGTCAAGATGGAATTTATGTCAAGAGTTGGCGCC 1832
Db      .....|||..... |||..... |||..... |||
321 ArgGluAspProGluPheProAspValSerSerGlyValPheValTyrGluValIleGln 340
QY      1833 AATTCACTTCTCAAGAGGCGCATCCAGATGATGATCAATCCAGTCAAGACGGG 1892
Db      .....|||..... |||..... |||..... |||
341 GlySerAlaIleAlaIleAspSerGlyLeuArgAspHisAspValIleValSerIleAsnGly 360
QY      1893 CGTCTCTAGTGAAGTCAAGTGAAGTCAAGAGCGCTGCTGACCGAGTCTCTCTCTTA 1952
Db      .....|||..... |||..... |||..... |||
361 GluProValThrThrThrThrAspValIleGluAlaValLysAspAsnAspPheLeuSer 380
QY      1953 CTGAGAGTGGCGGGGGAACAGACAGACTCTCTTCAGCATCGCACTGAGTGGTGC 2009
Db      .....|||..... |||..... |||..... |||
381 IleIleValLeuAspArgIleSerGlnThrLeuPheLeuThrValThrProGluIleIle 399

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RESULT 12

```

US-08-923-454A-6
/ Sequence 6, Application US/08923454A
/ Patent No. 6004794
/ GENERAL INFORMATION:
/ APPLICANT: Creasy, Caretha
/ APPLICANT: Livi, George
/ APPLICANT: Karran, Eric
/ APPLICANT: Clindenbeard, Helen
/ APPLICANT: Browne, Michael
/ APPLICANT: Southan, Christopher
/ TITLE OF INVENTION: HUMAN SERINE PROTEASE
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SmithKline Beecham Corporation
/ STREET: 709 Swedeland Road
/ CITY: King of Prussia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19406
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ Version 1.5
/ CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/08/923,454A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/025436
/ FILING DATE: 06-SEPT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Baumeister, Kirk
/ REGISTRATION NUMBER: 33,833
/ REFERENCE/DOCKET NUMBER: P50547
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5096
/ TELEFAX: 610-270-5090
/
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 423 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: N-terminal
/ ORIGINAL SOURCE:
/
US-08-923-454A-6
/
Alignment Scores:
/ Pred. No.: 1,32e-52 Length: 423
/ Score: 800.50 Matches: 197
/ Percent Similarity: 59.7% Conservative: 83
/ Best Local Similarity: 42.0% Mismatches: 103
/ Query Match: 14.4% Indels: 86
/ DB: Gaps: 14
/
US-10-617-443B-1 (1-3006) x US-08-923-454A-6 (1-423)
QY      680 GGGACAAACCCGAGATCCAGCCCGGCTCACTCCGTTGCTCAACGCAATATCTTAA 739
Db      .....|||..... |||..... |||..... |||
13 GlyArgArgProArgLeuThrProAspLeuArgAlaLeu-----LeuThrSer----- 28
QY      740 CCTCTCTGAGCGCTCTCCAGCCCTGACAGGAGTTCAGTGAAGGGGGGTGAGGAACCCA 799
Db      .....|||..... |||..... |||..... |||
29 GlyThrSerAspProArgAlaArgValThrTyr-----GlyThrPro 42
QY      800 GCACGTGGAAGCCTTTTAAACATTCTCGGGGTGAGAGCCCTTCCAAATGCTGGT 859
Db      .....|||..... |||..... |||..... |||
43 Ser-LeuTyrPalaArgLeuSerVal---GlyValIleGluPro--ArgAlaCysLeuThr 60
QY      860 GTCACTGACACTGCTGTGTGTAGGGGTGCC--CAACGGGCTCACTGAGGCTGAGGCT 916
Db      .....|||..... |||..... |||..... |||
60 rSer-----GlyThrProGluProArgAlaGlnLeu-----Thr 71
QY      917 GGCTTGAACCTGGAGAGGGGTTCAGAAAGACCTCTCTCTCCAGCTGGGATG 976
Db      .....|||..... |||..... |||..... |||
71 rAlaValThrProAspThrArgThrArgGluAlaSerGluAsnSerGlyThrArgSerArg 91
QY      977 G-----CCTGTGAGAGCTGCACAGCATCGATCTCACTGATG----- 1013
Db      .....|||..... |||..... |||..... |||
91 GalATrPLeuAlaValAlaLeuGlyAlaGlyAlaValLeuLeuLeuLeuTrpGly 111
QY      1014 -----CACCTGGCCCTTCCCGCAGCGGAGGTCTCCACCACTGACAGACGCCGCG 1063
Db      .....|||..... |||..... |||..... |||
111 yGlyArgGlyProProAlaValLeuAlaValAlaValProSerProProProAlaSerProArg 131
QY      1064 CTCAAGTTCAACTTCACTTCTGACGTGTGTGGAAGATCGACACGCGGTGTCACAT 1123
Db      .....|||..... |||..... |||..... |||
131 gSerGlnTyrAsnPheIleAlaAspValValGluLysThrAlaProAlaValValTyr 151
QY      1124 AGAGCTCTTCTGAGACACCGGCTGTTGGCCGCAACGTGCGCTGTCTGACGCGTTCTGG 1183
Db      .....|||..... |||..... |||..... |||
151 eGluIleLeuAspArgHisProPheLeuGlyArgGluValProIleSerAsnGlySerGly 171

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QY 1184 CTTTCATGATGTCAGAGGCGGCTGATCATCAATGCCAGCTGTTGTCAGCAACAG 1243
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Db 171 yPheValValAlaAlaAspGlyLeuValThrSerAlaValAlaAsp----- 189
QY 1244 TGCCTCCCGGCGAGGACAGCAAGTGCAGTCAAGAAATGGGACTCTCATAGAGC 1303
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 190 -----ArgArgArgValArgValArgLeuLeuSerGlyAspThrTyrGluAl 205
QY 1304 CACCATCAAGACATCGACAGAAAGTCCGACATTGCCACATCAAGATCCCAAGAA 1363
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 aValValThrAlaValAspProValAlaAspIleAlaThrLeuArgIleGlnThrLysGlu 225
QY 1364 AAAGCTCCCTGTTGTTGCTGAGTCACTCGGCGGACCTCGGCGGAGTTGTGTG 1423
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 225 uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyValLeuValVa 245
QY 1424 GGCCATCGGACATCCCTTCGCTTACAGAAACAGTGCACAGCGGATGTCAGCACTGC 1483
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 lAlaMetGlySerProPheAlaLeuGlnMetThrIleThrSerGlyIleValSerSerAl 265
QY 1484 CCAGCGGAGGAGGAGGAGCTGGGCTCGGGAATCCGACATGACTATCATCAAGCGA 1543
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 aGlnArgProAlaArgAspLeuGlyLeuProGlnThrAsnValGluTyrIleGlnThrAs 285
QY 1544 TGCCATCATCACTACGGGAGCTCGGCGGAGCACTGCGTGAACCTG----- 1589
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 285 pAlaAlaIleAspPheGlyAsnSerGlyLeuProLeuValAsnLeuAlaArgGluLeuGl 305
QY 1590 -----GATGCGAGGTCATTGGCATCAACAGCTCAAGTCAAGCTGAG 1633
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 305 yAlaValSerLeuGlnAspGlyGluValIleGlyValaLeuThrMetLysValThrAlaGl 325
QY 1634 CATTCCTCTTGGCATCCCTTCAGACCGCATCAACGCTTCTTCACAGATTCGAAAGAA 1693
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 325 yLleSerPheAlaIleProSerAspArgLeuArgGlnPheLeuAlaArgGlyGluLysVal 345
QY 1694 GCAG-----ATCAAAAGCTGGAAGAGCGCTTCACTCGGATCGATGCGAGC 1741
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 345 aAsnSerSerGlyLysSerGlySerGlnArgArgIleGlyValaMetMetLeuThr 365
QY 1742 GATCACACCAACCTGTCGATGATGATGAGCGGACCAAGCGGACTTCCAGAGGTGAG 1801
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 365 rLeuSerPro----- 368
QY 1802 CAGTGAATTATGTCAGAGAGGTGGCGGAATTCACCTTTCAGAGAGCGGCAATCCA 1861
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 -----ArgAlaGlyLeuArg 373
QY 1862 AGATGTGATCATCATCTGTCAGAGTCAACGGGCGTCTCTAGTGAATGAGTGAAGTGA 1921
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 373 gProGlyAspValIleLeuAlaIleGlyGlnGlnMetValGlnAsnAlaGlnAspValTy 393
QY 1922 GGAGGCGGTCGTCAGGAGTCTCTCTACTGAGAGTGGCGGCGGAGAAAGCAAGCACT 1981
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 393 rGluAlaValArgThrGlnSerGlnLeuAlaValGlnIleArgArgGlyArgGlnThrLe 413
QY 1982 CCTCTTACAGATCGACCTGAGGTG 2006
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Db 413 uThrLeuTyrValThrProGluVal 421

```

```

CORRESPONDENCE ADDRESS:
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
US-08-923-454A-29
Alignment Scores:
Pred. No.: 1,34e-52 Length: 436
Score: 800.50 Matches: 197
Percent Similarity: 59.7% Conservative: 83
Best Local Similarity: 42.0% Mismatches: 103
Query Match: 14.4% Indels: 86
DB: 2 Gaps: 14
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QY 680 GGAAGTAACCGAGATTCAGACCCCGGCTCACTCCGTTGCTACAGCGCAATATCTTA 739
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 26 GtArgArgProArgLeuThrProAspLeuArgAlaLeu-----LeuThrSer 41
QY 740 CCTCTCTGAGGCTCTCGCCAGCGCTAGCAGGCTCAGTAGAGGGGGGTGAGAAAGCCA 799
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 42 GtThrSerAspProArgAlaArgValThrTyr-----GlyThrPro 55
QY 800 GCACGTGGAAGCTTTTAACCATTCGCGGGTGAAGAGCCCTTCCCAATGCGCTGT 859
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 56 Ser-LeuThrPheAlaArgLeuSerVal---GlyValThrGluPro---ArgAlaCysLeuThr 73
QY 860 GTCACGTGCACTGCTGTGTGAGGGGATCCC---CAAGGGGCTCAGTGTGGGCTAGAGCT 916
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 rSer-----GlyThrProGlyProArgAlaGlnLeu-----Th 84
QY 917 GGCTCTGAAGTGGAGAGGGGTCTCAGGAAGAGCTCTCTCTGCGCCACTGGGCAATG 976
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 rAlaValThrProAspThrArgThrArgGlnAlaSerGlnLeuSerArgIleThrArgSerArg 104
QY 977 G-----CCTTGGAGCTGGCAGCATCTGATCTCAGTGAAG----- 1013
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 104 gAlaThrPheuAlaValAlaLeuGlyAlaGlyGlyValaValLeuLeuLeuLeuTyrGly 124

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1014 -----CACCTGGCCCTTCCCGCCGACGAGTCTCCACCAAGTACAGCCGCGG 1063
124 YGLIARGGLYPROPROLALAVALLAVALPROSERPROPROLALASERPROX 144
1064 CTACAAAGTTCAACTTCATTTGCTGACGTGTGAGAAAGATCCGACCGCGTGTCCACAT 1123
144 GserGlnYxanPheIleAlaAspValValGlnYThrAlaProAlaValValYrII 164
1124 AGAGCTCTTCTGAGACACCCGCTGTGTCGCGCAAGTCCCTGTGTCAGCGGTTCTGG 1183
164 eGlnIleuAspAlaPheIleAlaAspValValGlnYThrAlaProAlaValAlaAsp----- 202
1184 CTTTCATCATGTCAAGGCGCGGCTGATCATCATCCATGCCCGCGTGTGTCCAGCAACAG 1243
184 yPheValValAlaAlaAspGlyLeuIleValThrAlaAlaValAlaAsp----- 202
1244 TGCTGCCCGCGGACGACGAGTCAAGGTGACGACTACAGAAATGGGACTCTCATGAGGC 1303
203 -----ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 218
1304 CACCATCAAGACATGACAGAGATGCGACATTTGCCACCATCAAGATCCACCAAGA 1363
218 aValValThrAlaValAlaAspProValAlaAspIleAlaThrLeuArgIleGlnThrIle 238
1364 AAAGCTCCCTGTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
238 uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyGlnPheVal 258
1424 GGCCATCGGACAGTCCCTTGCCTTCCACAGAAACAGTGTGACACGGGATGTGTGACATCG 1483
258 lAlaMetGlySerProPheAlaLeuGlnAanThrIleThrSerGlyIleAlaSerIle 278
1484 CCAGCGGAGGCGGAGGAGTGGGCTCCGCGGACTCCGACATGAGTACTACATCCAGCGA 1543
278 aGlnArgProAlaArgAspLeuGlyLeuProGlnThrAsnValGlnYrIleGlnThrIle 298
1544 TGCCATCATCAACTACAGGGAATCTCCGCGGACCACTGGTGAACCTG----- 1589
298 pAlaAlaIleAspPheGlyAsnSerGlyGlyProLeuValAsnLeuAlaArgGlnLeu 318
1590 -----GATGGCGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1633
318 yAlaValSerLeuGlnAspGlyGlnValIleGlyValAsnThrMetIleValThrIle 338
1634 CATCTCTTGGCATCCCTTCCACAGACCGCATCAACAGGTTCTCTCAAGAGTTCCAAAGCA 1693
338 yIleSerPheAlaIleProSerAspArgLeuArgIlePheLeuAlaArgGlyGlnYrIle 358
1694 GCAG-----ATCAAAAGCTGGAAGAAAGGCTTCAATCCGATACGATACGATGCGAGC 1741
358 bAsnSerSerSerGlyIleSerGlySerGlnArgArgYrIleGlyValMetMetLeuThr 378
1742 GATTCACACCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1801
378 rLeuSerPro----- 381
1802 CAGTGAATTATATGCAAGAGTTCGCCGAATTCACCTTCAAGAGAGCGGACATCA 1861
382 -----ATGAlaGlyLeuAsr 386
1862 AGATGTGACATCATGATGATCAAGGCGCTCTCTAGTGAATCTGAGTGAAGTGTGCA 1921
386 gProGlyAspValIleLeuAlaIleGlyGlnMetValGlnAsnAlaGlnAspValYr 406
1922 GAGAGCGGTGTGACCGAGTCTCTCTCTCACTGAGAGTGTGCGCGGCGGAGAGACGACT 1981
406 rGlnAlaValAlaArgThrIleSerGlnLeuAlaValGlnIleArgArgIleArgGlnThrIle 426
1982 CTTCTTCAAGATCGACCTGAGGTG 2006
426 uThrLeuYrValThrProGlnVal 434

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RESULT 14
US-08-923-454A-27
Sequence 27, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karran, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-923-454A-27
Alignment Scores:
Pred. No.: 3,14e-36 Length: 377
Score: 585.50 Matches: 148
Percent Similarity: 63.9% Conservative: 56
Best Local Similarity: 46.4% Mismatches: 75
Query Match: 10.5% Indels: 40
Gaps: 11
US-10-617-443b-1 (1-3006) x US-08-923-454A-27 (1-377)
680 GGAGCTAACCGGAGATCAAGCCCGGCTCTCCGCTGTGCTCAAGGCAATATCTTAA 739
26 GYIARGGLYPROALALAVALLAVALPROSERPROPROALALASERPROX 41
740 CCTCTCTGTGAGCTCTCTCTCCACGACGATCAAGAGGTCCAGTGAAGGAGGTGAGGAAGCCA 739
42 GYIARGGLYPROALALAVALLAVALPROSERPROPROALALASERPROX 55
800 GCAGTGAAGCTTTTAACTTCTCGGAGTGAAGGAGCCCTTCCAAATGCTGT 859

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Db 56 Ser-LeuThrAlaArgLeuSerVal---GlyValThrGluPro---ArgAlaCysLeuThr 73
QY 860 GTCACTGCACTGCTGTGTGGGGGCTCC---CAACGGGCTCACTGTGGGCTGAGCT 916
Db 73 rSer-----GlyThrProGlyProArgAlaGlnLeu-----Th 84
QY 917 GCGCTGCAACTGGGACAGGGGCTCTGCAAGAGACGCTCTCTGCTGCCCACTGGGCAATG 976
Db 84 rAlaValThrProArgThrArgThrArgGlnAlaSerGluAenSerGlyThrArgSerAr 104
QY 977 G-----CCTTGGAGCTGGCAGCATCTGATCTCAATG----- 1013
Db 104 gAlaThrPleuAlaValAlaLeuGlyAlaGlyAlaValLeuLeuLeuLeuThrGlyGly 124
QY 1014 -----CACCTGGCCCTTCCCGGACAGCGAGGTCTCCACAGCTGAGCAGCCGGG 1063
Db 124 yGlyArgGlyProProAlaValLeuAlaValProSerProProProAlaSerProAr 144
QY 1064 CTACAAAGTTCAACTCATGCTGACGCTGGGAGAAATCGGACAGCCGCTGCTCAAT 1123
Db 144 gSerGlnTyraAsnPhelIleAlaAspValAlaGlnTyraAlaProAlaValAlaTyrl 164
QY 1124 AGAGCTCTTCTGAGACACCCGCTGTTTGGCCGCAACGTCGCCCTGTCAGCGGTTCTGG 1183
Db 164 eGluIleLeuAspArgHisProPheLeuGlyArgGluValProIleSerAsnGlySerG 184
QY 1184 CTTTCATCATGTGACAGGCGGCTGTATCTACCAATGCCCGACGCTGGTGTCCAGCAACG 1243
Db 184 yPheValValAlaAlaAspGlyLeuIleValThrAsnAlaHisValAlaAsp----- 202
QY 1244 TGCTGCCCCGGGACAGCAGCTCAAGGTGACAGAGTGCAGAGAGGGGAATCCTATGAGGC 1303
Db 203 -----ArgArgArgValArgValArgLeuLeuSerGlyAspThrTyrlGlnAl 218
QY 1304 CACCATCAAGAATCATGCAAGAGTGGACATTCGCAATTCAGATCCCAAGAA 1363
Db 218 aValValThrAlaValAlaAspProValAlaAspIleAlaThrLeuAlaGlnIleThrLysel 238
QY 1364 AAAGCTCCCTGTTGTTGTTGCTGGGTCACTGGCCGACCTGGCCGCTGGGGAAGTTGTGT 1423
Db 238 uProLeuProThrLeuProLeuGlyArgSerAlaAspValArgGlnGlyGluPheValVa 258
QY 1424 GGCCATCGGAGCTCCCTGCGCTTACAGAAACAGTGAAGGGGAGATGTCAGACATGC 1483
Db 258 lAlaMetGlySerProPheAlaLeuGlnAsnThrIleThrSerGlyIleValSerSerAl 278
QY 1484 CCAGCGGAGGAGGAGGAGCTGGGCTCCGGGACTCCGACATGCAATGCAATCCAGACGA 1543
Db 278 aGlnArgProAlaArgAspLeuGlyLeuProGlnThrAsnValGlnTyrlIleGlnThrAs 298
QY 1544 TGCCATCATCACTACGAGGAACTCCGGGGGACCACTGGTGAACCTGGATGGCGAG 1598
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RESULT 15
US-08-923-454A-4
Sequence 4, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasey, Carantha
APPLICANT: Livi, George
APPLICANT: Karan, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA

ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Discrete
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923.454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGIN: SOURCE:
US-08-923-454A-4

Alignment Scores:
Pred. No.: 1,09e-35 Length: 323
Score: 578.00 Matches: 134
Percent Similarity: 66.7% Conservative: 46
Best Local Similarity: 49.6% Mismatches: 62
Query Match: 10.4% Indels: 28
Gaps: 7

US-10-617-443B-1 (1-3006) x US-08-923-454A-4 (1-323)

QY 825 CTCGGGGTGGAGGAGCCCTTCCCAATGCTGTGTACTGCACTGCTGTGTGAGG 884
Db 9 ValGlyValThrGluPro---ArgAlaCysLeuThrSer-----Gly 21
QY 885 GGTCCC---CAACGGGCTCAGTGTGGGCTGAGGCTGCTGAACTGGGACAGGGGCTGC 941
Db 22 ThrProGlyProArgAlaGlnLeu-----ThrAlaValThrProAspThrArgThr 38
QY 942 AGGAAGACCTCTCTCTGCTGCCCACTGGGCAATGAG-----CCTTGGGA 986
Db 39 ArgGluAlaSerGluAenSerGlyThrArgSerArGlnAlaThrPleuAlaValAlaLeuGly 58
QY 987 GCTGGACACATGTCATCTCATG-----CACCTGGCCCTTCCC 1028
Db 59 AlaGlyGlyAlaValLeuLeuLeuLeuThrGlyGlyArgGlyProProAlaValLeu 78
QY 1029 GCCAGCGAGGTCTCCACACCTGACGAGCCCGGCTCAAGTTCAATTCATGCTGCTGAC 1088
Db 79 AlaAlaValProSerProProProAlaSerProArgSerGlnTyraAsnPhelIleAlaAsp 98
QY 1089 GTGTGGAGAAATGCAACAGCCGCTGCTCAATAGCTCTTCTGAGACACCCGCTG 1148
Db 99 ValValGlnTyraAlaProAlaValAlaValTyrlIleGluIleLeuAspArgHisProthe 118
QY 1149 TTTGGCCGCAACGTGCCCTGTCTCAAGCGGTTGCTTCATCATGTCAAGAGCCGGCTG 1208
Db 119 LeuGlyArgGluValProIleSerAsnGlySerGlyPheValAlaAlaAlaAspGlyLeu 138
QY 1209 ATCATCACCAATGCCCAAGTGTGTCCAGCAAGTGTGCCCGGCGGACAGCAGAGCTC 1268

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 21, 2006, 20:45:26 ; Search time 83.2 Seconds
(without alignments)
3019.219 Million cell updates/sec

Title: US-10-617-443B-1

Perfect score: 5578
Sequence: 1 caggagaccgcgaagttgcag.....gccaaaaaaaaaaaaaa 3006

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
MODE=frame+np.model -DEV=xlp
-O=/abs/ABSSWB/spool/US10617443/runat_21022006_165448_15797/app_query.fasta_1
-DB=Published Applications AA Main -QFMT=fastaan -SUFFIX=n2p.rabpm
-MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0 -UNITS=bits -SPART=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NOR=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs802p
-USER=US10617443@CGN 1 1 307 @runat_21022006_165448_15797 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: Published Applications AA Main:*
2: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1679	30.1	334	4	US-10-189-099A-2 Sequence 2, Appl1
2	1679	30.1	334	5	US-10-617-443B-2 Sequence 2, Appl1
3	1668	29.9	453	3	US-09-796-753-32 Sequence 12, Appl1
4	1668	29.9	453	4	US-10-275-505-14 Sequence 14, Appl1
5	1668	29.9	453	4	US-10-381-820A-8 Sequence 8, Appl1
6	1668	29.9	453	5	US-10-485-313A-33 Sequence 13, Appl1
7	1668	29.9	453	6	US-11-140-224-14 Sequence 14, Appl1
8	1638	29.4	348	3	US-09-796-753-34 Sequence 34, Appl1
9	1554	27.9	459	5	US-10-485-313A-27 Sequence 27, Appl1
10	1546.5	27.7	452	4	US-10-301-822-79 Sequence 79, Appl1
11	1378	24.7	286	3	US-09-764-898-256 Sequence 256, Appl1

12	1150	20.6	357	5	US-10-485-313A-34 Sequence 34, Appl1
13	1121	20.1	330	3	US-09-764-898-184 Sequence 184, Appl1
14	1075	19.3	363	5	US-10-485-313A-39 Sequence 39, Appl1
15	1060.5	19.0	480	4	US-10-170-385-355 Sequence 355, Appl1
16	1060.5	19.0	517	5	US-10-772-636-48 Sequence 48, Appl1
17	1054.5	18.9	480	4	US-10-264-049-2310 Sequence 2310, Appl1
18	1043.5	18.7	447	4	US-10-104-047-2765 Sequence 2765, Appl1
19	1000	17.9	405	3	US-09-925-298-552 Sequence 552, Appl1
20	1000	17.9	405	4	US-10-102-806-552 Sequence 552, Appl1
21	903.5	16.2	458	3	US-09-968-418-11 Sequence 11, Appl1
22	903.5	16.2	458	4	US-10-197-634-1 Sequence 1, Appl1
23	903.5	16.2	458	4	US-10-180-719-11 Sequence 11, Appl1
24	903.5	16.2	458	4	US-10-352-684A-10 Sequence 10, Appl1
25	903.5	16.2	458	6	US-11-045-577-11 Sequence 11, Appl1
26	903.5	16.2	529	3	US-10-216-667-5 Sequence 5, Appl1
27	902	16.2	476	3	US-09-935-390A-37 Sequence 37, Appl1
28	902	16.2	476	4	US-10-789-241-50 Sequence 50, Appl1
29	902	16.2	476	5	US-10-772-636-8 Sequence 8, Appl1
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33	882	15.8	321	5	US-10-730-476A-52 Sequence 52, Appl1
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35	866	15.5	325	4	US-10-730-476A-45 Sequence 45, Appl1
36	866	15.5	325	5	US-10-730-476A-47 Sequence 47, Appl1
37	866	15.5	325	5	US-10-730-476A-45 Sequence 45, Appl1
38	866	15.5	325	5	US-10-730-476A-46 Sequence 46, Appl1
39	866	15.5	325	5	US-10-730-476A-47 Sequence 47, Appl1
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41	862	15.5	325	5	US-10-730-476A-53 Sequence 53, Appl1
42	854	15.3	178	4	US-09-969-384-18 Sequence 18, Appl1
43	696	12.5	225	4	US-10-730-476A-48 Sequence 48, Appl1
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ALIGNMENTS

RESULT 1
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; Sequence 2, Application US/10189099A
; Publication No. US20040005659A1
GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Oi, Jian-shen
; APPLICANT: Chen, Cailin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/189,099A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-099A-2

Alignment Scores:
Pred. No.: 7,486-98
Score: 1679.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 30.1%
DB: 4
Gaps: 0

US-10-617-443B-1 (1-3006) x US-10-189-099A-2 (1-334)

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QY      1491 GAGGCGAGGAGCTGGGCTTCGGGATTCGCACTGAGATCAATCCAGACGATGCCATC 1550
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; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/617,443B
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 334
; TYPE: PRP
; ORGANISM: Homo sapiens
US-10-617-443B-2

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Score: 1679.00 Matches: 334
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 30.1% Indels: 0
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Dd		452	Iwet 453	
 RESULT 4 US-10-275-505-14 Sequence 14, Application US/10275505 Publication NO. US20040081961A1 GENERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC. APPLICANT: DELEGANE, Angelo M.; IAL, Preeti G. APPLICANT: HAFELIA, April J.A.; PATTERSON, Chandra APPLICANT: WALTA, Narinder K.; KEANEY, Liam APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A. APPLICANT: YAO, Monique G.; BAUSHN, Marian R. APPLICANT: AZIMZAI, Yalda; ELLOT, Vicki S. APPLICANT: NGUYEN, Danielle B.; GANDHI, Ameena R. APPLICANT: YANG, Junming; HERNANDEZ, Roberto APPLICANT: POLICKY, Jennifer L.; LU, Dyoung Aina M. APPLICANT: REDDY, Roopa M.; YUE, Henry APPLICANT: TANG, Y. Tom TITLE OF INVENTION: PROTEASES FILE REFERENCE: PI-0085 USN CURRENT APPLICATION NUMBER: US/10/275_505 CURRENT FILING DATE: 2002-11-04 PRIOR APPLICATION NUMBER: PCT/US01/14651 PRIOR FILING DATE: 2001-05-04 PRIOR APPLICATION NUMBER: 60/209,402 PRIOR FILING DATE: 2000-06-01 PRIOR APPLICATION NUMBER: 60/207,477 PRIOR FILING DATE: 2000-05-25				

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Qy	1409	TGGGAGATTGTGGGGCCATGGGAGTCCCTCCGCCCAAGAACAGTCAACAGG	1460
Db	252	CGIyIuPheValValAlaIleGlyIleAsnThrleuGlnAsnThrValThrThr	272
Qy	1469	CATCTGCAGACTGCCCGACCGGAGGCGGAGGAGTGGGCTCCGGACCTCCGACATGGA	1528
Db	272	YIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAs	292
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Qy	1709	GAAGAGCGCTTCATCGGCATACGAGTGCAGATCAACCAAGCTGTGTGATGAGCT	1768
Db	352	plyLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuValAspGluLe	372
Qy	1769	GAAGGCCAGCAACCCGGACTTCCCAAGGTCAAGCATGTGAATTTATGTCCAGAGTTGC	1828
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Qy	1829	GCCGAATTCACCTTCTCAGAGAGGCGGCATCCAAAGTGTGACATCATCTGCAAGGTCAA	1888
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Qy	1889	CGGGCGTCTCTTAGTAGACTCGAGTAGCTGCAGAGGCGGTGCTGACCGAGTCTTCTCT	1948
Db	412	nglyArgProLeuValAspSerSerGluLeuGlnGluAlaValleuThrGluSerProle	432
Qy	1949	CCTACTGGAGGTGGCGCGGGGGAAGACGACTCTCTTCAGACATCGCACTGAGGTGGT	2008
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Db	452	lMet 453	
RESULT 5			
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: Sequence 8, Application US/10381820A			
: Publication No. US20040142333A1			
: GENERAL INFORMATION:			
: APPLICANT: Deshun, Lu			
: APPLICANT: Song, Ho Yeong			
: APPLICANT: Su, Eric Wen			
: APPLICANT: Wang, He			
: TITLE OF INVENTION: Novel Secreted Proteins and Their Uses			
: FILE REFERENCE: X-13974			
: CURRENT APPLICATION NUMBER: US/10/381,820A			
: CURRENT FILING DATE: 2003-03-27			
: NUMBER OF SEQ ID NOS: 8			
: SOFTWARE: PatentIn version 3.2			
: SEQ ID NO 8			
: LENGTH: 453			
: TYPE: PRT			
: ORGANISM: Homo sapiens			
US-10-381-820A-8			
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Pred. No.:	3,97e-97	Length:	453

[illegible]


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QY      1829  GCCGAATTCACCTTCTCAGAGAGGCGGACATCAAGTGTGACATCATGTCAGGTCA 1888
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QY      1889  CGGGGCTCTCTAGTGCATCGAGTGCAGAGGCGGTGTCAGCCGAGTCTCTCT 1948
Db      412  nGlyArgProIeuValAspSerSerGluIeuGlnIleValIeuThrGluSerProIe 432
QY      1949  CTTACTGAGAGTGGCGGGGGGAGACAGACATCTCTTTCAGCATGCGACCTGAGGTGT 2008
Db      432  uIeuIeuGlnValArgArgGlyAsnAspAspIeuPheSerIleAlaProGlnValIva 452
QY      2009  CATG 2012
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RESULT 7
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; Sequence 14, Application US/11140224
; Publication No. US20050227280A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G.
; APPLICANT: HAPALIA, April J.A.; PATTERSON, Chandra
; APPLICANT: MALA, Nandinder K.; KEARNEY, Liam
; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.
; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
; APPLICANT: AZIMZAI, Yalda; ELLIOTT, Vicki S.
; APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.
; APPLICANT: YANG, Junming; HERNANDEZ, Roberto
; APPLICANT: POLICKY, Jennifer L.; LU, Dyrung Aina M.
; APPLICANT: REDDY, Roopa M.; YUE, Henry
; APPLICANT: TANG, Y. Tom
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0085 USN
; CURRENT APPLICATION NUMBER: US/11/140,224
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/10/275,505
; PRIOR FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: PCT/US01/14651
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/209,402
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/207,477
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/205,803
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: 60/203,566
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: 60/202,082
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PERL Program
; SEQ ID NO 14
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7474343CD1
US-11-140-224-14

Alignment Scores:
Pred. No.: 3,97e-97 Length: 453
Score: 1668.00 Matches: 354
Percent Similarity: 79.0% Conservative: 11
Best Local Similarity: 76.6% Mismatches: 30
Query Match: 29.9% Indels: 67
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US-10-617-443B-1 (1-3006) x US-11-140-224-14 (1-453)

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Db      44  ValProAspIeu-CysAsnCysCysIeuValCysAlaAlaSerGluGluProCysGly 63
QY      884  GGGTCCCAACGGGGTCTGAGTGGGCTGAGGCTG-----GCTCT 922
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Db      83  sArgTrpSerHisAlaValCysGlyThrAspGlyHisThrTyrAlaAsnValCysAlaIle 103
QY      942  -----AGGAAGGCTCTCTCTCTCTCTGCGCCATGAGGCGATGAGGCTGTGGAGC 988
Db      103  uGlnAlaAlaSerArgArgAlaIeuGlnIeuSerGlyThrProValArgGlnIeuGlnIly 123
QY      989  TGGCAGCATCGTGCATCTGATGATGATGACCTGGCCCTTCCGCGCAGCGACGTCTCCACCA 1048
Db      123  sGlyAlaCysProIeu-----GlyIeuHisIle 132
QY      1049  GCTGAGCAGCCCGGCTCAAACTTCACTTCACTTCACTGAGAGAGATGCGAC 1108
Db      132  nIeuSerSerProArgTyrIlyPheAsnIleAlaAspValIleAlaValIleAlaIly 152
QY      1109  AGCCGTGTCTCCATAGAGCTCTTCTGAGACACCGGCTTGGCCGCGAAGTGGCCCT 1168
Db      152  AlaValAlaHisIleGluIeuPheIeuArgHisProIeuPheGlyArgAsnValProIe 172
QY      1169  GTCCAGCGGTTCTGCTTCATCATGTCAGAGCGCGGCTGATCATCACCAGTCCACGT 1228
Db      172  uSerSerGlySerGlyPheIleIleMetSerGluIleGlyIeuIleIleThrAsnAlaHisIle 192
QY      1229  GGTGTCCAGCAACAGTGTGTCGCCCGGAGGAGGAGGAGCTCAAGGTGACGTCACAGATGG 1288
Db      192  lValSerSerAsnSerAlaAlaProGlyArgGlnGlnIeuIlyValGlnIeuGlnIleAsn 212
QY      1288  GGACTCTCTATGAGGCCACATCAATGAAGATGAGAGTGGACATTTGCCACATCA 1348
Db      212  yAspSerTyrGlnAlaThrIleIlyAspIleAspIlySerAspIleAlaThrIleIly 232
QY      1349  GATTCATCCCAAGAAAGAGTCCCTGTGTGTGCTGGGCTACTGCGCGACCTCGGCGC 1408
Db      232  sIleHisProIlySlySlySlyIeuProValIeuIeuIeuGlyHisSerAlaAspIeuArgPr 252
QY      1409  TGGGAGATTGTGTGTGTCATCGGAGTCCCTTGCCTTCAAGAACACAGTGAACAGGG 1468
Db      252  cGlyIeuPheValIleAlaIleGlySerProIleAlaIeuGlnIleAsnThrValThrThrGly 272
QY      1469  CATGCTGACACTGCCACGCGGAGGAGGAGGAGGAGCTGCGGCTCCGAGCATGGA 1528
Db      272  yIleValSerThrAlaGlnArgGlnIlyArgGluIeuGlyIeuAspSerAspMetAs 292
QY      1529  CTACATCCAGACGAGTGCATCATCACTACGGAAGTCCGGGGAGACCTGTAACCT 1588
Db      292  pTyrIleGlnThrAspAlaIleIleAsnIlyGlyIeuSerArgGlyProIeuValAsnIle 312
QY      1589  GGATGCGAGAGTCATTTGCGATCAACACGTCAGAGTCAAGGCTGCGCATCTCTTGCCAT 1648
Db      312  uAspGlyIleValIleGlyIleAsnThrIeuIlyValThrAlaGlyIleSerPheAlaIle 332
QY      1649  CCCCTCAGACCGCATCAACAGGTTCTCTCAACAGAGTTCACAGACAGATCAAGACG 1708
Db      332  eProSerAspArgIleThrArgPheIeuThrGluPheGlnIleAspIlyGlnIleIlyAspTr 352
QY      1709  GAAAGAGCGCTTCATCGGATACGATGCGAGTGGAGCATCAACAGCTGTGATGATGAGCT 1768

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Db 352 p|y|e|y|s|a|g|p|h|e|i|l|e|y|i|l|e|a|r|g|m|e|t|a|g|r|h|i|l|e|h|p|r|o|s|e|r|i|e|u|l|a|s|p|g|u|l|e| 372
Qy 1769 g|a|a|g|c|c|a|g|c|c|c|g|a|c|t|c|c|c|a|g|g|t|c|a|g|t|g|a|a|t|t|a|t|g|t|c|a|a|g|g|t|g|c| 1828
Db 372 u|l|y|s|a|l|a|s|e|r|a|s|p|r|o|p|h|e|r|p|r|o|g|i|u|l|a|l|s|e|r|s|e|r|g|i|l|e|t|y|r|v|a|l|g|i|n|l|u|l|a|l| 392
Qy 1829 g|c|c|g|a|t|t|c|c|t|t|c|a|g|a|g|c|c|g|c|c|a|a|g|a|g|t|g|a|t|c|t|c|t|c|a|a|g|g|t|c|a| 1888
Db 392 a|p|r|o|h|a|n|s|e|r|p|r|o|s|e|r|i|n|r|g|i|l|y|i|l|e|g|i|n|a|s|g|i|l|a|s|p|i|l|e|i|l|e|l|u|l|y|s|v|a|l|a| 412
Qy 1889 c|c|g|c|c|g|t|c|t|c|t|a|g|t|g|a|c|t|c|a|g|t|g|a|c|t|g|a|g|c|c|g|t|c|t|g|a|c|c|g|t|c|t|c|t| 1948
Db 412 n|o|l|y|a|r|p|r|o|l|e|u|l|a|l|a|s|p|r|e|r|s|e|r|g|i|u|l|e|u|g|i|n|l|u|l|a|l|e|u|h|t|r|c|i|u|s|r|p|r|o|l|e| 432
Qy 1949 c|c|t|a|c|t|g|a|g|t|c|c|g|c|c|g|g|g|a|a|c|g|a|c|c|t|c|t|c|t|t|c|a|g|a|t|c|c|a|g|t|g|t| 2008
Db 432 u|l|e|u|g|i|u|l|a|l|a|r|g|r|g|i|l|y|a|n|a|s|p|a|s|p|l|e|u|l|e|u|h|p|h|e|s|e|r|i|l|e|a|i|p|r|o|g|i|u|l|a|l|a| 452
Qy 2009 c|a|n|g| 2012
Db 452 l|w|e|t| 453

RESULT 8
US-09-796-753-34
; Sequence 34, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
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; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 34
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Mouse
US-09-796-753-34
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Alignment Scores:

	pred. No.:	2,99e-95	length:	348
Score:		1638.00	Matches:	330
Percent Similarity:		97.1%	Conservative:	2
Best Local Similarity:		96.5%	Mismatches:	8
Query Match:		29.4%	Indels:	2
DB:		3	Gaps:	1

US-10-617-443b-1 (1-3006) x US-09-796-753-34 (1-348)

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Qy 987 g|c|t|g|g|a|g|a|t|c|g|a|t|t|c|a|g|t|g|a|c|c|t|g|c|c|g|c|c|a|g|c|c|a|g|t|t|c|c|a|c| 1046
Db 9 s|e|r|g|i|y|t|h|r|p|r|o|v|a|l|a|r|g|i|n|l|e|u|g|i|n|l|y|s|i|g|i|a|c|y|p|r|o|-----l|e|u|i|l|e|u|h|i|s| 26
Qy 1047 c|a|g|t|g|a|g|a|c|c|c|g|c|t|a|c|a|g|t|t|c|a|a|g|t|t|c|t|g|a|g|t|g|t|g|a|a|a|t|c|c|g|a| 1106
Db 27 g|i|n|l|e|u|s|e|r|p|r|o|r|g|r|y|r|y|s|p|h|e|a|n|p|h|e|i|l|e|a|s|p|a|l|a|l|u|l|y|r|i|l|e|a|l|a| 46
Qy 1107 c|c|a|g|c|c|g|t|g|t|c|c|a|t|a|g|t|t|c|t|g|a|g|a|c|c|c|g|t|t|t|g|g|c|c|g|a|c|g|t|g|c|c| 1166
Db 47 p|r|o|l|a|l|a|l|a|l|h|i|s|i|l|e|i|l|e|u|h|e|u|h|g|h|i|s|r|p|r|o|l|e|h|e|i|l|a|r|g|r|a|n|l|a|l|p|r|o| 66
Qy 1167 t|g|t|c|c|a|g|c|g|t|t|g|g|t|t|c|t|t|c|a|t|g|t|c|a|g|g|c|c|g|c|c|t|g|a|t|c|a|c|c|a|t|g|c|c|a|c| 1226
Db 67 l|e|u|s|e|r|s|e|r|g|i|s|e|r|c|i|y|h|e|i|l|e|m|e|s|e|r|g|i|u|a|i|g|i|l|e|i|l|e|h|r|a|n|l|h|i|s| 86
Qy 1227 g|t|g|t|g|t|c|c|a|g|a|c|a|g|t|g|t|c|c|c|c|g|c|c|g|c|c|a|g|c|c|a|g|t|c|c|a|g|t|t|c|c|a|g|a|t| 1286
Db 87 v|a|i|l|a|s|e|r|s|e|r|a|n|s|e|r|i|a|l|a|p|r|o|g|i|a|r|g|i|n|l|e|u|l|y|v|a|i|g|i|n|l|e|u|i|n|a|n| 106
Qy 1287 g|g|g|a|c|t|c|t|a|g|a|g|c|c|a|c|a|t|c|a|a|a|g|a|c|t|g|a|a|g|t|c|c|a|c|a|t|c| 1346
Db 107 g|i|y|a|s|p|r|e|r|t|y|c|i|u|l|a|h|a|r|h|i|l|e|y|s|a|r|i|l|e|a|r|y|s|y|s|e|r|a|s|p|i|l|e|h|a|h|r|i|l|e| 126
Qy 1347 a|a|g|a|t|c|a|t|c|c|a|a|a|a|a|a|g|t|c|c|t|g|t|g|t|g|t|g|t|g|t|g|t|g|t|g|t|g|t|g|t|g|t|g|t|g|t| 1406
Db 127 l|y|s|i|l|e|h|i|a|r|p|r|o|l|y|e|l|y|s|e|u|h|e|u|p|r|o|v|a|i|l|e|u|h|e|u|g|i|n|h|i|s|e|r|i|l|a|s|p|r|e|u|a|r|g| 146
Qy 1407 c|c|t|g|g|a|g|t|t|g|t|g|t|g|c|c|a|t|c|c|g|c|a|t|c|c|c|t|t|c|c|c|t|a|c|a|a|a|c|a|c|a|t|g|c|a|a|g| 1466
Db 147 p|r|o|g|i|y|g|i|u|h|p|h|e|v|a|i|a|l|a|l|e|g|i|s|e|r|p|r|o|h|e|i|a|l|e|u|h|a|n|h|r|a|i|l|h|r|h|r| 166
Qy 1467 g|c|c|a|t|g|t|c|a|g|a|c|t|g|c|c|a|g|g|g|a|g|g|c|a|g|g|a|g|t|g|g|c|c|t|c|c|g|g|a|c|t|c|c|a|c|a|t|g| 1526
Db 167 g|i|y|i|l|e|v|a|l|e|s|e|r|t|h|r|a|i|n|g|i|n|r|g|i|u|l|e|u|g|i|l|e|u|h|a|r|g|s|p|r|e|r|h|a|n|h|e|c| 186
Qy 1527 g|a|c|t|a|c|a|t|c|c|a|g|c|c|a|t|c|c|a|t|c|a|c|t|n|a|c|g|g|a|a|c|t|c|c|g|g|g|a|c|c|a|c|t|g|t|g|a|a|c| 1586
Db 187 a|s|p|r|y|r|i|l|e|g|i|n|h|r|a|s|p|a|i|l|e|i|l|e|a|n|t|y|r|g|i|y|a|n|s|e|r|g|i|g|i|y|r|p|r|o|l|e|u|v|a|i|a|n| 206
Qy 1587 c|t|g|a|t|g|c|g|a|g|t|a|t|t|g|g|c|a|t|c|a|c|a|c|c|t|c|a|a|g|t|c|a|c|g|c|t|g|g|c|a|t|c|c|t|t|g|g|c| 1646
Db 207 l|e|u|a|s|p|g|i|y|g|i|u|l|a|i|l|e|i|l|y|l|e|a|n|h|r|l|e|u|l|y|v|a|i|h|a|i|g|i|l|y|l|e|s|e|r|h|e|i|a| 226
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QY 1647 ATCCCTCAGACCGGATCAACAGGTTCTCAGAGATTCCAGAGATCAAGACAGATCAAGAC 1706
DB 227 ILeProserAspArgIleThrArgPheLeuThrGluPheGlnAspIleGlnIleYsAsp 246
QY 1707 TGGAGAGACGCTTTCATCGGCATACGGATGCGAGACATCAACCAAGCTGTGTGATGAG 1766
DB 247 TrpYsIlyAspArgPheIleGlyIleArgMetArgThrIleThrProSerLeuValAspGlu 266
QY 1767 CTGAAGGCGCAGAACCCCGGACTTCCAGAGGTCCAGAGTGAAGTATTAATGCAAGGTT 1826
DB 267 LeuYsAlaSerAspProAspPheProGluValSerSergIlyIleYrValGlnGluVal 286
QY 1827 GCGCCGAATTCACTTCTCAGAGAGCGGCATCAAGATGTGACATCGTCAAGTCC 1886
DB 287 AlaProAsnSerProSerGlnArgIlyGlyIleGlnAspGlyAspIleIleValIlySVal 306
QY 1887 AACGGCGCTCTCTAGTGAAGCTCGAGTGAAGCTGCAAGAGCGCTGTGTCAGGATCTCT 1946
DB 307 AsnGlyArgProLeuValAspSerSergIleGlnGluValIleValLeuThrGluSerPro 326
QY 1947 CTCCTACTGAGAGTCCGGCGGGGGAACGACGACCTCTCTTACAGATCGACATGAGTGC 2006
DB 327 LeuLeuLeuGluValAlaArgArgIlyAsnAspAspLeuLeuPheSerIleAlaProGluVal 346
QY 2007 GTCATG 2012
DB 347 ValMet 348

RESULT 9
US-10-485-313A-27
; Sequence 27, Application US/10485313A
; Publication No. US2005005902A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiying
; APPLICANT: SALMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-485-313A-27

Alignment Scores:
Pred. No.: 6,69e-90 Length: 459
Score: 1554.00 Matches: 329
Percent Similarity: 76.4% Conservative: 24
Best Local Similarity: 71.2% Mismatches: 42
Query Match: 27.9% Indels: 67
DB: 5 Gaps: 7

US-10-617-443B-1 (1-3006) x US-10-485-313A-27 (1-459)
QY 749 GAGCCTCTGCTCCAGCCTAGACAGGGTCCAGTGAAGGGGGGTGAGAGAACCCAGACGTGGA 808
DB 25 GluProAlaAlaPro-----CysProAlaArgCys 35
QY 809 AGCCTTTTAACATTCCTCGGGGTGAGAGCCCTTCC-----CAA 850
DB 36 AspAl-----SerArgCysProSerProArgCysProGlyGlyTyr 49
QY 851 ATGCTGTGTCTACTGACGTGCTGTGTGTA-----GG 883

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DB 50 ValProAspLeu-CysAsnCysCysLeuValCysAlaAlaSerGluGlyGluProCysIle 69
QY 884 GGGTCCCAACCGGCTCAGTGTGGCTGAGGCTG-----GCTCT 922
DB 69 YArgProLeuAspSerProCysGlyAspSerLeuGluCysValArgGlyValCysArgCys 89
QY 923 GAACGTGGAGCAGGGGCTTC----- 941
DB 89 sArgThrThrHisThrValCysGlyThrAspGlyHisThrTyrAlaAspValCysAlaLe 109
QY 942 -----AGGAAGCCTCTCTCTCTCTGCGCCACTGGGCAATAGGCTCTGGAGAC 988
DB 109 uGlnAlaAlaSerAspArgAlaLeuGlnValSerGlyThrProValArgGlnLeuGlnIly 129
QY 989 TGGCAGCATTCGTATCTCACTGATGCACCTGAGCTGCGCTTCCCGCAGCGCAGGTCTCCACCA 1048
DB 129 sGlyAla-----CysProSergIlyLeuHisIleG 138
QY 1049 GCTGAGCAGCCCGGCTCAAGTTCACTTCACTGACCGTGGAGAGAGATGCGACCC 1108
DB 138 nLeuThrSerProArgTyrIlyAspAspPheIleAlaAspValValGluYsIleAlaIyr 158
QY 1109 AGCCGTGTCCACATAGAGCTCTTCTGAGACACCGGCTGTTGGCCGCAAGTCCCT 1168
DB 158 cAlaValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProle 178
QY 1169 GTCCAGCGGTTCTGGCTTCATCATGTCAGAGCGGCTGATCATCACCATGCCACGT 1228
DB 178 uSerSergIlySergIlyPheIleMetSergIlyAlaGlyLeuIleValThrAsnAlaHisVal 198
QY 1229 GGTGTCCAGCAACAGTGTGCCCCGGGAGAGAGAGCTCAAGGTGCAGTCTCAGAAATG 1288
DB 198 lValSerSerSerThrAlaSerGlyArgGlnGlnLeuYsValGlnLeuGlnAsnI 218
QY 1289 GAACTCTATAGAGGCAACCATCAAGACATGACACAAGATGCGACATTTGCCACATCA 1348
DB 218 yAspAlaTyrGluAlaThrIleGlnAspIleAspYsSerAspIleAlaThrIleVal 238
QY 1349 GATCCATCCCAAGAAAAGCTCCGTGTGTGTGCTGGGTCACTCGGCGACCTCGCGGC 1408
DB 238 lIleHisProIlySylSylSleuProValLeuLeuLeuGlnHisSerAlaAspLeuArgyr 258
QY 1409 TGGGAGTTTGTGTGGCCATCGGACATCCCTTGCCTTACAGAACACAGTGAACAAGGG 1468
DB 258 cGlyGlnPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThxI 278
QY 1469 CATGTCAGCACTGCCAGCGGAGGAGGAGGAGCTCGGACTCCGAGACTCCGACATGGA 1528
DB 278 yIleValSerThrAlaGlnArgAspGlyLyGluLeuGlyLeuArgAspSerAspMetAs 298
QY 1529 CTACATCCAGACGATGCGATCATCAACTACGGGAATCCGGGGAGCACTGTGTAACT 1588
DB 298 pTyrIleGlnThrAspAlaIleIleAsnTyGlyAsnSergIlyProLeuValAsnIle 318
QY 1589 GAATGCGAGGTCTTGGCATCAACAGCTCAAGGTCAAGGTGCGATCTCTTTGCCAT 1648
DB 318 uAspGlyGluValIleGlyIleAsnThrLeuYsValAlaIleGlyIleSerPheAlaI 338
QY 1649 CCCCTCAGACCGCATCACAGGGTCTCTCAGAGTTCACAGACAGACAGATCAAGACTG 1708
DB 338 eProSerAspArgIleThrArgPheLeuSerGluPheGlnAsnYsHisValYsAspTr 358
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QY 1769 GAAGCGCAACCCCGACTTCCAGAGTTCAGACAGTGCAGATTTATGTGCAAGAGTTGC 1828
DB 378 uYsAlaAlaAsnProAspPheProAlaValSerSergIlyIleYrValGlnGluValVa 398
QY 1829 GCCGAATTCACCTTCAAGAGAGCGGACATCAAGATGTGATCAATCATGTCAGAGTCAA 1888

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: TITLE OF INVENTION: Nucleic Acids, proteins, and Antibodies
:
: FILE REFERENCE: P3201
: CURRENT APPLICATION NUMBER: US/09/764,898
: PRIORITY FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 311
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 184
: LENGTH: 330
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (244)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: NAME/KEY: SITE
: LOCATION: (255)
: OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
: US-09-764-898-184

Alignment Scores:
Pred. No.: 1,72e-62 Length: 330
Score: 1121.00 Matches: 241
Percent Similarity: 75.5% Conservative: 32
Best Local Similarity: 73.0% Mismatches: 8
Query Match: 20.1% Indels: 49
DB: Gaps: 4

US-10-617-443B-1 (1-3006) x US-09-764-898-184 (1-330)

QY 791 GGAAAGCCGAGCATGTGAGACCTTTTAAACCATTCCTCGGGGCTGAGAGAGCCCTTCCCA 850
D 18 GlySerProGly-LeuGlnGlnPheGlyThrSerAlaSerGluGlyPro----- 34
QY 851 ATGCGGTGTCATCGCATCGCTGTGTGGTAGGGGGTCCCAACGGGCTCACTGTGGGCT 910
D 35 -----GlyGlyGlyProLeuAlaPheProCysGlyG 45
QY 911 GAGGCTG-----GCTGTGAACTGGGAAGGGGTCTC----- 941
D 45 uSerLeuGluCysValArgGlyLeuCysArgCysArgTyrSerHisAlaValCysGlyTh 65
QY 942 -----AGCAAGAGCTCTCT 955
D 65 rAlaPglyHisThrTyrAlaAsnValCysAlaLeuGlnAlaAlaSerArgAlaLeuG 85
QY 956 CCTCTGCGCCACTGGGCGCATAGAGCTCTGGGAGCTGGGAGCATGTCATCTCACTGATGCA 1015
D 85 nLeuSerGlyThrProValArgGlnLeuGlnGlyGlyValCysProLeu----- 101
QY 1016 CTTGGGCTTCCCGCGAGCGCAGGCTCTCCACAGCTGAGCAGCGCCGGCTTCAAGATTGA 1075
D 102 -----GlyLeuHisGlnLeuSerSerProArgTyrLysPheAs 114
QY 1076 CTTGATTGCTGACGTGTGTGAGAAAGATGGACACAGCGGTGTCCACATAGAGCTTTCTT 1135
D 114 nPheLeuAlaAspValValGlnLysLeuLeuProAlaValAlaHisIleGlnLeuPhe 134
QY 1136 GAGAGCACCGCGCTGTTGGCGCGCAACGTGCCCTGTCCAGCGGTTTGGCTTCATCAATGTC 1195
D 134 uArgHisProLeuPheGlyArgAsnValProLeuSerSerGlySerGlyPheIleMetSe 154
QY 1196 AGAGGCGGCGCTGATCATCAACCAATGCCAAGCGGTGTCAGCAACAAGTGTGCGCCGGG 1255
D 154 rGluAlaGlyLeuLeuIleThrAsnAlaHisValValSerSerAsnSerAlaAlaProG 174
QY 1256 CAGGAGAGAGTCAAGGTGACGTACAGAAATGGGGACTCTTATGAGGCCACCATCAAGA 1315
D 174 yArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAs 194
QY 1316 CATGCACAAAGATTCGAGCATTCGACCATCAAGATTCATCCCAAGAAAAAGCTCCCTGT 1375
D 194 rLeuAspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLeuLeuProVa 214

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QY 1376 GTTGTGCTGGGCTCACTCGGCGGAGCTGGGCGCTGGGAGTTTGTGGTGGCCATCGGCG 1435
DB 214 lIeunleuenglYhIsSerIaAspIeunrProglYgluPheValAlaIlelYSe 234
QY 1436 TCCCTTCCGCTTACAGAACACAGTGAACAAGGAGCATTCGACAGCTGCGGAGGAGG 1495
DB 234 rProhealAleuEngInaenThrValThr**GlyIleValSerThrAlaGlnArgGlu 254
QY 1496 CAGGAGCTGGGCTTCGGGAGCTCCGACATGAGCTACATCCAGACCGATGCAATCA 1555
DB 254 YArgIleuEngIlyLeuArgAspSerAspMet**TyrIleGlnThrAspAlaIleIleAs 274
QY 1556 CTAACGGAACTCCGGGGGAGCACTGTGAACCTGATGGCGGAGTTCGATGCAAC 1615
DB 274 nTyrGlyAsnSerGlyGlyProleuValAsnleuAspGlyIleGlyIleAsnTh 294
QY 1616 GCTCAAGCTCAGCGCTGCGATCTCTTTCGATCCCTCAGACCGCATCAGCGTTCT 1675
DB 294 rIeunYsValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPhe 314
QY 1676 CACAGAGTTCCAAGACACAGCATCAA 1703
DB 314 uThrGluPheGlnAspIyGlnIlelYs 323

RESULT 14
US-10-485-313A-39
; Sequence 39, Application US/10485313A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiying
; APPLICANT: SALAMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 39
; LENGTH: 363
; TYPE: PR
; ORGANISM: Mus musculus
US-10-485-313A-39

Alignment Scores:
Pred. No.: 1,45e-59 Length: 363
Score: 1075.00 Matches: 234
Percent Similarity: 71.3% Conservative: 22
Best Local Similarity: 65.2% Mismatches: 36
Query Match: 19.3% Indels: 67
DB: 5 Gaps: 7

US-10-617-443B-1 (1-3006) x US-10-485-313A-39 (1-363)
QY 749 GAGCTCTCTCCGACGCTGACAGGCTCCAGTGAAGGGGGGTGAAGAACCCCAAGCATGGA 808
DB 25 GluProProAlaAlaPro-----CysProAlaArgCys 35
QY 809 AGCCTTTTAAACATTCTCGGGGTAGCGAGCCCTTTC-----CAA 850
DB 36 AspVal-----SerArgCysProSerProArgCysProGlyTyr 49
QY 851 ATGCGTGTGTCACTGCACTGCTGTGTGTA-----GG 883
DB 50 ValProAspLeu-CysAsnCySerLeuValCysAlaIleSerGluGlyGluProCysG 69

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QY 884 GGGTCCCAAGCGGCTCATGTGAGGCTGAGGCTG-----GCTCT 922
DB 69 YArgProleuAspSerProCysGlyAspSerleuGluCysValArgGlyValCysArgCys 89
QY 923 GAATGGAGCAGGGCTC----- 941
DB 89 sArgTrpThrIleThrValCysGlyThrAspGlyHisThrTyrAlaAspValCysAlaIle 109
QY 942 -----AGGAAGAGCTCTCTCTCTCTGCGCACTGGGAGTAAAGCTTGGAGC 988
DB 109 uGlnAlaIleAspArgAlaIleuGlnValSerGlyThrProValArgGlnleuGly 129
QY 989 TGGCAGCATTCGATCTCATGTATGATGACCTGGCCCTCCCGCAGCGAGGTCTCCACCA 1048
DB 129 sGlyAla-----CysProSerGlyLeuHisG 138
QY 1049 GCTGAGACCCCGGCTCAAGTTCAACTTCAATGCTGACGTGTGAGAGAGATGCAACC 1108
DB 138 nleuThrSerProArgTyrIlyPheAsnPheIleAlaAspValValGluYsIleAlaPr 158
QY 1109 AGCGTGTCCCATAGAGCTCTTCTGAGACACCCGCTGTTGGCCGCAAGTCCCT 1168
DB 158 oAlaValAlaHisIleGluLeuPheLeuArgHisIleProleuPheGlyArgAsnValProle 178
QY 1169 GTCCAGCGGCTTCTGCTCATCATGTCAAGAGCGGCGCTGATCATCACCAATGCCACGT 1228
DB 178 uSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleValIleThrAsnAlaHisVa 198
QY 1229 GGTGTCCAGCAACAGTGTGCCCCCGGAGGAGGAGCTCAAGTGCAGCTACAGAAATG 1288
DB 198 lValSerSerSerSerThrAlaSerGlyArgGlnGlnleuYsValGlnleuGlnAsnG 218
QY 1289 GAGCTCTTATGAGGCGCACCATTAAGACATGACACAAAGTGGACATTCGCCACATCA 1348
DB 218 YAspAlaTyrGluAlaThrIleGlnAspIleAspIlySerAspIleAlaThrIleVa 238
QY 1349 GATCATCCCAAGAAAGAGCTCCGTGTGTGTGGGTCTACGTGGCGGACCTCGGCG 1408
DB 238 lIleHisProIySlySlySleProValleuIleuIleuGlyHisSerAlaAspLeuArgPr 258
QY 1409 TGGGAGGTTTGTGTGAGCATGCGGAGTCCCTTCCGCTTACAGAACACAGTGAACGG 1468
DB 258 oGlyGluPheValValAlaIleGlySerProhealAleuGlnAsnThrValThrG 278
QY 1469 CATGCTCAGCACTGCCAGCGGAGGAGGAGGAGCTCGGAGCTCCGACATGGA 1528
DB 278 YIleValSerThrAlaGlnArgAspGlyIyGlyIleuGlyLeuArgAspSerAspMetAs 298
QY 1529 CTACATCCAGAGAGTGCATCATCACTACAGGAACTCCGGGGGAGCCAGTGTGAACCT 1588
DB 298 pTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProleuValAsnle 318
QY 1589 GGATGGCGAGGCTATTTGACATCAACAGCTCAAGGCTCAAGGCTGACATCTCTTGGCAT 1648
DB 318 uAspGlyGluValIleGlyIleAsnThrleuYsValAlaIleGlyIleSerPheAlaI 338
QY 1649 CCCCTCAAGCGGATCAACAGGTTCTTCAAGAGTTCACAGACACAGCATCAA 1703
DB 338 eProSerAspArgIleThrArgPheLeuSerGluPheGlnleuYHisValIys 356

RESULT 15
US-10-170-385-355
; Sequence 355, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart

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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 21, 2006, 20:48:06 ; Search time 4.1 Seconds
(without alignments)
2088.023 Million cell updates/sec

Title: US-10-617-443B-1

Perfect score: 5578
Sequence: 1 cagggactcgaagtttcag.....gccaaaaa.....3006

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 108093 segs, 14239677 residues

Total number of hits satisfying chosen parameters: 216186

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Published Applications_AA_New -OPMT=faeacan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=hits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MILEN=0
-MAXLEN=200000000 -HOST=abs802p
-USER=US10617443@cgn1_1_7/runac_21022006_165450_15843 -NCPU=6 -ICPU=3
-NO MAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications_AA_New.*

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6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1546.5	27.7	452	7	US-11-186-284-79 Sequence 79, Appl
2	1060.5	19.0	480	6	US-10-821-234-1465 Sequence 1465, Ap
3	1043.5	18.7	447	7	US-11-072-512-2765 Sequence 2765, Ap
4	903.5	16.2	458	7	US-11-183-914-11 Sequence 11, Appl
5	535	9.6	109	7	US-11-053-076-59 Sequence 59, Appl
6	496	8.9	100	7	US-11-107-096-78 Sequence 78, Appl
7	425	7.6	474	7	US-11-098-686-10591 Sequence 10591, A
8	424.5	7.6	499	6	US-10-467-657-2096 Sequence 2096, Ap
9	387	6.9	441	6	US-10-454-437-56 Sequence 56, Appl

10	335.5	6.0	423	7	US-11-074-176-4 Sequence 4, Appl1
11	318	5.7	317	6	US-10-793-626-1824 Sequence 1824, Ap
12	309.5	5.5	1717	7	US-11-182-016-20 Sequence 20, Appl
13	309	5.5	1466	7	US-11-186-284-33 Sequence 33, Appl
14	293.5	5.3	1166	6	US-10-821-234-964 Sequence 964, Appl
15	277.5	5.0	1742	7	US-11-182-016-23 Sequence 23, Appl
16	266.5	4.8	1717	7	US-11-182-016-20 Sequence 20, Appl
17	262	4.7	1733	7	US-11-182-016-21 Sequence 21, Appl
18	260.5	4.7	493	6	US-10-793-626-1832 Sequence 1832, Ap
19	259.5	4.7	115	6	US-10-485-788A-774 Sequence 774, App
20	259.5	4.7	115	6	US-11-053-076-152 Sequence 152, App
21	254.5	4.6	1496	7	US-11-186-284-35 Sequence 35, Appl
22	251.5	4.5	1733	7	US-11-182-016-21 Sequence 21, Appl
23	248	4.4	1464	7	US-11-186-284-28 Sequence 28, Appl
24	248	4.4	1464	7	US-11-021-603-2 Sequence 2, Appl1
25	248	4.4	1467	6	US-10-821-234-1096 Sequence 1096, Ap
26	247	4.4	1464	7	US-11-000-463-243 Sequence 243, App
27	245.5	4.4	1377	6	US-10-821-234-1070 Sequence 1070, Ap
28	245	4.4	1823	6	US-10-995-561-988 Sequence 988, App
29	245	4.4	2102	6	US-10-995-561-990 Sequence 990, App
30	245	4.4	2157	6	US-10-995-561-991 Sequence 991, App
31	243.5	4.4	1464	7	US-11-000-463-243 Sequence 243, App
32	243.5	4.4	1464	7	US-11-186-284-28 Sequence 28, Appl
33	243.5	4.4	1464	7	US-11-021-603-2 Sequence 2, Appl1
34	243.5	4.4	1467	6	US-10-821-234-1096 Sequence 1096, Ap
35	242	4.3	2108	6	US-10-995-561-989 Sequence 989, App
36	239	4.3	101	7	US-11-107-096-77 Sequence 77, Appl
37	235.5	4.2	1730	7	US-11-182-016-19 Sequence 19, Appl
38	233.5	4.2	1874	6	US-10-821-234-1182 Sequence 1182, Ap
39	233	4.2	1767	6	US-10-995-561-911 Sequence 911, App
40	233	4.2	1767	6	US-10-995-561-914 Sequence 914, App
41	233	4.2	1806	6	US-10-995-561-912 Sequence 912, App
42	233	4.2	1806	6	US-10-995-561-915 Sequence 915, App
43	233	4.2	1818	6	US-10-995-561-910 Sequence 910, App
44	233	4.2	1818	6	US-10-995-561-913 Sequence 913, App
45	231.5	4.2	1742	7	US-11-182-016-23 Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-11-186-284-79
Sequence 79, Application US/11186284
Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kametkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John B.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
FILE REFERENCE: MP001-029P2RM
CURRENT APPLICATION NUMBER: US/11/186,284
PRIORITY FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301,822
PRIORITY FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIORITY FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 452
TYPE: PR
ORGANISM: Homo Sapiens


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Db      61 -----AlaCys-----GlyCysGlyValCysGlyAlaProGluGlyAla 74
Qy      678 GGG---GGAGTAAACCCGAGATCCAGCCCCGCGCTCACTCCGCTGGCTCAACGCAATAT 734
Db      75 AlaCysGlyLeuGlnGluGlyProCysGlyGlyGluGlnCys----- 89
Qy      735 CCTAACCTCTCTAGAGCTCTGCTCCGACCCAGGAGGCTCAAGTGAAGGGGGGTGAGAA 794
Db      90 -----ValValPro-----PheGlyValProAlaSerAlaThrVal 101
Qy      795 GCCCAGCAGCTGGAAGCCTTTTAAACATTTCTGGGGGTGAGCGAGCGCTTCCCAATGC 854
Db      102 ArgAlaGAlaGlnAlaGlyLeuCysValCysAlaSerSerGluProAla----- 118
Qy      855 CTGGTGTCACTGCACTGCTGTGTGTGTAGGGGGTCCCAACGGGCTCAAGTGTGGCTGAG 914
Db      119 -----CysGlySerAlaAlaThrValAlaAsnLeuCysGlnLeuArg 133
Qy      915 CTGGCTGTGAATGGGACAGGGGTCTCAAGGAAGCCTCTCTCTGCGCCACTGGGCT 974
Db      134 AlaAla-----SerArgArgSerGluArgLeu-----His 143
Qy      975 AGGCTCTGGAGAGTGGCAGCATCGTATCTGATCTGATGCACTGGGCTTCCCGCCAGC 1034
Db      144 ArgPro-----ProValIleValLeuGlnArgGlyAla-----CysGly 156
Qy      1035 GCAAGCTTCCACAGCTGAGCAGCCCGCGCTCAAGTTCACTTCACTTGTGAGTGTG 1094
Db      157 GlnGlnGlnGlnAlaProAlaValAlaIleGlnLeuPheArgLeuProPheSerIle 176
Qy      1095 GAGGAAGATGGCAGCAGCCTGGTCCCATATAGCTTCTTCTGAGACACCCGCTGTTGGC 1154
Db      177 GlnValIleAlaProAlaValAlaIleGlnLeuPheArgLeuProPheSerIle 196
Qy      1155 CGCAACGCTCCCTGCTCCAGCGGTTCTGAGCTTCACTGATCAAGGCGCGCTGATCATC 1214
Db      197 ArgGluValAlaProValAlaSerGlySerGlyPheIleValSerGluAspIleVal 216
Qy      1215 ACCAATGCCACGTGTGTCCAGCAAGCTGCTCCCGCGGAGCGAGCACTCAAGTGTG 1274
Db      217 ThrAlaAlaIleValIleValThrAsn-----LysHisArgValIleVal 230
Qy      1275 CAGCTACAGAAATGGGGATCCCTATAGAGCGCAACATCAAGATCAAGCAAGATCGGAC 1334
Db      231 GlnLeuLysAsnGlyAlaThrTyArgIleValIleValAspValAspIleValAsp 250
Qy      1335 ATTGGCACCATCAAGATCCATCCCAAGAAAGATCCCTGTGTGTGTGTTGGGTCACTG 1394
Db      251 IleAlaLeuIleLeuIleAlaPheIleGlnGlyLeuLeuProValLeuLeuGlnArgSer 270
Qy      1395 GCCGACCTGGCGCTGGGAGATTGTGTGTGGCCATGGGAGTCCCTTCCGCTCAAGAAC 1454
Db      271 SerGlnLeuArgProGlyGlnPheValIleAlaIleGlySerProPheSerLeuGlnAsn 290
Qy      1455 ACAAGTGAACAAGGGGATGCTGACCACTGCCACGCGGAGGAGGAGGAGCTGGGCTCCGG 1514
Db      291 ThrValIleThrGlyIleValIleSerThrGlnArgGlyGlyLysGlnLeuGlyLeuArg 310
Qy      1515 GACTCCGACATGAGATCAATCCAGACGAGTGCATATCAATCAATCAAGGAACTCCGGGGGA 1574
Db      311 AsnSerAspMetCaspArgIleGlnIleThrAspAlaIleIleAsnArgIleAsnSerGlyGly 330
Qy      1575 CCAGTGTGAACCTGTGATGGAGGATCATTTGGCATCAACAGCTCAAGGTCAAGCTGGC 1634
Db      331 ProLeuValAlaAsnLeuAspIleGlyValIleGlyIleAsnThrLeuLysValIleThrAlaGly 350
Qy      1635 ATCTCTTTGGCATCCCTCAACCGCATCAACAGGTTCTTCAACAGATTCCAAAGCAAG 1694
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Qy      1746 ACACCAAGCTCTGTGATGAGTGAAGTGAAGCCAGCAACCCGAGTTTCCCAAGGTCAAGT 1805
Db      391 ThrSerSerLysAlaLysGlnLeuLysAspArgHisAspAspPheProAlaIleSer 410
Qy      1806 GGAATTTATGTGCAAGAGGTTGCGCGAATTCACTTCTCAGAGAGCGCGCATCCCAAGAT 1865
Db      411 GlyAlaTyrlleIleGlnValIleProAspThrProAlaGlnAlaGlyLysLeuVal 430
Qy      1866 GGTGACATCATGTCAGAGTCAACGGCGCTCTAGTGAATCGAGTCAAGTCAAGTCAAGAG 1925
Db      431 AsnAspValIleIleSerIleAsnGlyGlnSerValIleSerAlaAsnAspValIleSer 450
Qy      1926 GCCGTGCTACCGAGATGCTCTTCTCACTGAGAGTGGCGGGGGAACGACGATCCCTTC 1985
Db      451 ValIleLysArgGlnSerThrLeuAsnMetValValAlaArgGlyAsnGlnAspIleMet 470
Qy      1986 TTCAGCATCGACATGAGGTGCTC 2009
Db      471 IleThrValIleProGlnLeuIle 478

RESULT 3
US-11-072-512-2765
; Sequence 2765, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TERSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHITO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2765
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2765

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Percent Similarity: 65.1%
Best Local Similarity: 50.1%
Query Match: 18.7%
DB: 7
Gaps: 14

US-10-617-443B-1 (1-3006) x US-11-072-512-2765 (1-447)
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IMMEDIATE SOURCE:
LIBRARY: SINICT01
CLONE: 2680548
US-11-183-914-11

Alignment Scores:

Pred. No.:	1,52e-47	Length:	458
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QY 740 CCTCTCTGAGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 42 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 800 GACGCTGAGAGCTTTTAACTTCTCGGGTGAAGCGAGCCCTTCCCAATGCTGTGT 859
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 56 Ser-LeuThrAlaArgLeuSerVal---GlyValThrGluPro---ArgAlaCysLeuThr 73
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DB 73 rSer-----GlyThrProGlyProArgAlaGlnLeu-----Th 84
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 917 GGCTTGAAGTGGGACAGGGGTCTCAGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTGATG 976
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 84 rAlaValThrProAspThrArgThrArgGluAlaSerGluAsnSerGlyThrArgSerAr 104
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 977 G-----CCTCTGGAGAGCTGGACAGCACTCGATCTCATGATG----- 1013
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 104 GAlaThrPheLeuAlaValAlaLeuGlyAlaGlyValAlaValLeuLeuLeuThrGlyGly 124
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1014 -----CACCTGGCCCTTCCCGCCAGCCGACAGGTCTTCCACAGCTGAGCAGCCCGCG 1063
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 124 YGlyArgGlyProProAlaValLeuAlaValAlaProSerProProAlaSerProAr 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1064 CTACAGATTCATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1123
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 144 SerGlnThrAspPheLeuAlaAspValAlaGluThrAlaProAlaValAlaValAlaVal 164
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1124 AGAGCTCTCTGAGACACCCGCTGTTTGGCCGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCT 1183
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 164 eGluLeuLeuAspArgHisProPheLeuGlyArgGlyValAlaProLeuSerHisGlySerG 184
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1184 CTTCATCATGTGACAGGCGGCTGATCATCAACCAATGCCAGCTGCTGCTGCTGCTGCTGCTGCT 1243
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 184 YPheValValAlaAlaAspGlyLeuAlaValAlaThrAlaAlaHisValAlaAlaAsp----- 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1244 TGCTGCCCCGGGACGAGCAGCTCAAGTGCAGCTACAGCAATGGGAGATCTCTATGAGGC 1303
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 203 -----ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1304 CACCTCAAAAGACATTCAGCAAGAGTGGCATTCGACCATCAATCAATCATCCCAAGAA 1363
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 218 aValValThrAlaValAlaAspProValAlaAlaPheLeuAlaThrLeuAlaGlyLeuThrLysG 238
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1364 AAAGTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 238 uProLeuProThrLeuProLeuGlyArgSerAlaAspValAlaGlnGlyGluPheValAla 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1424 GGGCATGGGACATCTTCTGCTTACAGAAACAGTGAAGAGGAGATGTGTACAGCATTC 1483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 258 lAlaMetGlySerProPheAlaLeuGlnAsnThrIleThrSerGlyIleValSerSerAl 278
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1484 CAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 278 aGlnArgProAlaArgAspLeuGlyLeuProGlnThrAsnValGluThrLys 298
QY 1544 TGCCATCATCACTACGGGAATCCCGGGGAGACCATTTGGTGAACCTTGAGAGAGTCTAT 1603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 298 rAlaAlaLeuAspPheGlyAsnSerGlyGlyProLeuValAlaLeuAspGlyGluVal 318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1604 TGCCATCAACAGCTCAAGGTACAGGCTGAGCTGCTCTTGGCATCCCTCAGAGCGCAT 1663
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 318 eGlyValAsnThrMetCysValThrAlaGlyIleSerPheAlaIleProSerAspArgLe 338
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1664 CACAGGTTCTCTCAGAGATTCCAAACACAGCAG-----ATCAAGACTGGAA 1711
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 338 uArgGluPheLeuHisArgGlyGluLysValAsnSerSerGlyIleSerGlySerG 358
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1712 GAAGGCTTCACTCGGCATACGATGCGGACCATCAACCAACCTGCTGATGAGCTGTA 1771
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 358 nArgArgThrIleGlyValAlaMetMetLeuThrLeuSerProSerIleLeuAlaGluLeuG 378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1772 GGCCAGCAACCCGAGCTTCCAGAGGTGACAGTGAATTTATGTGCAAGAGTTGCGCC 1831
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 nLeuArgGluProSerPheProAspValGlnHisGlyValLeuIleHisLysValIleLe 398
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1832 GAATTCACCTTCTCAGAGAGCGGACATCCAGATGATGATGATGATGATGATGATGATGAT 1891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 398 uGlySerProAlaHisArgAlaGlyLeuArgProGlyAspValIleLeuAlaIleGlyG 418
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1892 GCGTCTCTAGTGAAGTCAAGTCAAGAGCCGCTGCTGACGAGTCTCTCTCT 1951
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 418 uGlnMetValGlnAlaAlaGluAspValThrValAlaValAlaArgThrGlnSerGlnLeuAl 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1952 ACTGAGAGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2006
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 438 aValGlnIleArgArgGlyArgGluThrLeuThrLeuThrValThrProGluVal 456
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
US-11-053-076-59
; Sequence 59, Application US/11053076
; Publication No. US20050255460A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Somoza Diaz-Sarmiento, Chamorro
; APPLICANT: Belmares, Michael P.
; TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
; FILE REFERENCE: VITA-008CIP
; CURRENT FILING DATE: 2005-02-07
; PRIOR FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: PCT/US03/28508
; PRIOR FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: 60/490,094
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: 60/450,464
; PRIOR FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: 60/409,298
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/630,590
; PRIOR FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 10/080,273
; PRIOR FILING DATE: 2002-02-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 109
; TYPE: PRT

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: ORGANISM: Homo sapiens			
US-11-053-076-59			
Alignment Scores:			
Pred. No.:	1,94e-25	Length:	109
Score:	535.00	Matches:	106
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	9.6%	Indels:	0
DB:	7	Gaps:	0
US-10-617-443B-1 (1-3006) x US-11-053-076-59 (1-109)			
QY	1674	CTCACAGAGTTCCACAGACAGATCAAGACTGGAAGACCGCTTCATGCGCATACG	1733
DB	1	LEUTHRGLPNHCINASPYSGLILEYASPTPLSLYSAPGHEIILEIYLLEARG	20
QY	1734	ATGCGACGATCACACCAAGCCTGTGTGATGAGCTGAAGCCGACCAACCCGACTTCCA	1733
DB	21	MeatqTnrlleThProSerleuValAspGluLeuLYaLaserAnProAspHePro	40
QY	1794	GAGGTTCACAGCTGAATTTATATGCAAGAGTTGGCCGGAATTCCTTTCAAGAGGC	1833
DB	41	GUValSerSeGlyIleTyrvAlGInGUValAProAsSerProSerGlnArgGly	60
QY	1854	GGCATCCAAAGATGTGACATCATCGTCAAGGTCAACGGGCGCTCTAGTGAATCGAGT	1913
DB	61	GIYlIeGInAspGlyAspIleIleVallybValaenGlyArgProLeuValAspSer	80
QY	1914	GAGCTGCAGAGAGCCGTGCTGACCGAGTCTCTCTCTACTGAGAGTGGCGGGGCAAC	1973
DB	81	GIueuGInGUValAValleuThrgIuSerProLeuLeuGUValAArgGlyAsn	100
QY	1974	GACGACTCTCTTCAGC	1991
DB	101	AspAspLeuLeuPheSer	106
RESULT 6			
US-11-107-096-78			
: Sequence 78, Application US/11107096			
: Publication No. US20060003348A1			
: GENERAL INFORMATION:			
: APPLICANT: SIDHU, SACHDEV S.			
: TITLE OF INVENTION: OMI PDZ MODULATORS			
: FILE REFERENCE: P2100R1			
: CURRENT APPLICATION NUMBER: US/11/107,096			
: CURRENT FILING DATE: 2005-04-15			
: PRIOR APPLICATION NUMBER: US 60/563,157			
: PRIOR FILING DATE: 2004-04-16			
: NUMBER OF SEQ ID NOS: 79			
: SEQ ID NO 78			
: LENGTH: 100			
: TYPE: PRT			
: ORGANISM: Homo sapiens			
US-11-107-096-78			
Alignment Scores:			
Pred. No.:	4.27e-23	Length:	100
Score:	496.00	Matches:	100
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	8.9%	Indels:	0
DB:	7	Gaps:	0
US-10-617-443B-1 (1-3006) x US-11-107-096-78 (1-100)			
QY	1713	AAGCGCTTCATCGGATACGAGATGCGAGCATACCAAGCCTGTGATGAGCTGAAG	1772
DB	1	LYsArgPHeIleGlyIleArgMeChArgThrlleThProSerleuValAspGluLeuYs	20
QY	1773	GCGAGCAACCGGACTTCCACAGAGGTCAAGCTGAATTTATGTGCAAGAGTTGCGCG	1832

Db	21	AlaSerAenPProAepPheProGluValSeretGlyIleTyRValGIngluValAlaPro	40
Qy	1833	AAATTAACCTTCTCAGAGAGCGGACATCCAGATGATGATCATCATGTCACAGCGG	1892
Db	41	AenSerProSerGInArgGlyIleGInAepGlyAepIleIleValIyValAenGly	60
Qy	1893	CGTCTCAAGAGACTCGAGTACGTGAGAGCGCGTGCAGACCAAGTCCCTCTCTCTA	1952
Db	61	ArgProLeuValAapSerSerGluLeuGInLValIValLeuTrnGluSerProLeu	80
Qy	1953	CTGAGAGTGCAGCGCGGGAGACAGCACTCTCTTTCAGATCGACCTGAGGTGATG	2012
Db	81	LeuGluValArgArgGlyAenAapAepPheSerIleAlaProGluValValMet	100
RESULT 7			
US-11-098-686-10591			
/ Sequence 10591, Application US/11098686			
/ Publication No. US20060024696A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Kapur, Vivek and Gebhart, Connie J.			
/ TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES			
/ TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING			
/ FILE REFERENCE: 09531-128001			
/ CURRENT APPLICATION NUMBER: US/11/098, 686			
/ CURRENT FILING DATE: 2005-04-04			
/ PRIOR APPLICATION NUMBER: PCT/US03/31318			
/ PRIOR FILING DATE: 2003-10-01			
/ PRIOR APPLICATION NUMBER: US 60/416,395			
/ PRIOR FILING DATE: 2002-10-04			
/ NUMBER OF SEQ ID NOS: 11433			
/ SOFTWARE: FastSeq for Windows Version 4.0			
/ SEQ ID NO 10591			
/ LENGTH: 474			
/ TYPE: PRT			
/ ORGANISM: Lawsonia intracellularis			
US-11-098-686-10591			
Alignment Scores:			
Pred. No.: 8,71e-19 Length: 474			
Score: 425.00 Matches: 138			
Percent Similarity: 45.9% Conservative: 83			
Best Local Similarity: 28.6% Mismatches: 173			
Query Match: 7.6% Indels: 88			
DB: 7 Gaps: 17			
US-10-617-443B-1 (1-3006) x US-11-098-686-10591 (1-474)			
Qy	978	CCTCTGGGAGTGGACAGATGATGATCTCACTGACATGCACTGGCCCTTCCCGACAGGCA	1037
Db	21	ProThrIleAlaGluSerAlaLeuProAenPheValIProLeuValIyAapAlaSerLys	40
Qy	1038	GGTCTCCACCAAGCTGAGCAGC-----CCGCGCTACAAGTTCAACTTCATTGCT	1085
Db	41	AlaValValAenIleSerThrGluLysLysIleProArgGlyArgTrnGluPhePromet	60
Qy	1086	GACGTGGTGGAGAAAGATCGACCAAGCGGTGTCACATAGAGCTTTCCTG-----	1136
Db	61	GluMetPheArgGlyLeuProProGly-----PheGluArgPhePheGluInPhe	77
Qy	1137	-----AGACACCGCGCTGTTGGCCGACAGCGTGCCTTGTCCAGCGGTTCTGCTTCATC	1190
Db	78	GluProLysGlyProAapSerGInIleHisLysGInArgSerLeuGlyTrnGlyPheIle	97
Qy	1191	ATGTCAAGAGCGCGGCTGATCATCAACCAATGCCACGTGTGTTCCAGAAACATGCTGCC	1250
Db	98	IleSerSerAepGlyTyIleValThrAaAenHisValIleGlu-----	112
Qy	1251	CCGGGAGGACGACGAGCTCAAGGTGCACACTCAG-----AATGGGACTCCTAT	1298
Db	113	---GlyAlaAepSerValArgValAaenLeuGluIyThiSerGlyLysGluSerLeu	131
Qy	1399	GAGGCGCACATCAAAAGACATGACCAAGAGTGGACATTGCCACCATCAAGATTCATCC	1358

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Db      132 ProAlaGluValIleGlyArgAspGluGluThrAspLeuAlaLeuLeuValValysSer 151
Qy      1359 AAGAAAAGCTCCCTGTGTTGCTGGGTCACTGGCCGACCTGGCGCTGGAGTTT 1418
Db      152 LysAspSerLeuProTyrLeuIlePheGlyAsnSerAspThrMetIuValGlyGluTrp 171
Qy      1419 GTGGTGGCCATCGGAGCTCTTCCGCTACAGAAAGATGACGAGCAACGGGACCTGGCAGC 1478
Db      172 ValLeuAlaIleGlyAsnProPheGlyLeuGlyHisThrValThrAlaGlyIleLeuSer 191
Qy      1479 ACTGCCAGCGGAGGAGGAGGAGCTGGGCTCCGGAGCTCCGACATGAGTACATCCAG 1538
Db      192 Ala-----LysGlyArgAspIleHisAlaGlyProPheAsp---AsnPheLeuGln 207
Qy      1539 ACGGATGCCATCATCACTACCGGAACTCCGGGGAGCCATGTGTAACCTGGATGGCGAG 1598
Db      208 ThrAspAlaSerIleAsnProGlyAsnSerGlyGlyProLeuIleAsnMetSerGlyGln 227
Qy      1599 GTCATTTGGCATCAACGCTCAAGGTCACGCGCT-----GGCATCTCTTTGCCATCCCC 1652
Db      228 ValValGlyIleAsnThrAlaIleMetAlaSerGlyGlnGlyIleGlyPheAlaIlePro 247
Qy      1653 TCAGACCGCATCACACGGTTCTCTCAGAGTTCCAGACAGACAGATCAAGACTGGAG 1712
Db      248 SerSerMetAlaAspArgIleIleGlyGlnLeu-----LysThrAsnLysValSer 265
Qy      1713 AAGCCCTCATCTGGCATACGATGCGGAGCATCAACCAAGCTGTGGATGAGTGAAG 1772
Db      266 ArgGlyTyrPileGlyValThrIleGlnAspValAspThrAlaValAlaLeuGly 285
Qy      1773 GCCCAACACCGGACTTCCAGAGGTGACAGTGAATTATGTGCAAGAGGTGGCGCG 1832
Db      286 LeuSerGln-----AlaLysGlyAlaLeuValGlySerValValPro 299
Qy      1833 AATTCACTTCTCAGAGAGCGGATCCAAAGTGTGATCATCATCAAGGTCAACGGG 1892
Db      300 GlyAspProAlaAspIleGlyValLeuValGlyAspIleValThrGlnAlaAspGly 319
Qy      1893 CGTCTCTAAGTGAAGTCCAGTGAAGTGCAGAGGCGGTCTGACGAGCTCTCTCTCA 1952
Db      320 LysGlnIleAspSerAlaSerSerLeuLeuValAlaIleAlaThrLysProPro----- 337
Qy      1953 CTGAGAGTGGCGGCGGGAACAGACGACCTCTCTGACATGCGACCTGAGGTGGCTAG 2012
Db      338 -----PheSerValValLysLeuValValTrp 346
Qy      2013 TGAGGGGCGCATCTCTCCAGCGCCAGCGCTCAGAGCTTGACAGCAACGAGGCGAGCGCC 2072
Db      347 -----ArgAspGlyLysSerLysAspIleSerIleThrLeuGlyGlnArg 361
Qy      2073 CCCCCGAGATCAGACGAAGACACCGTGGTCTCTCAGACGAGGCGGCGACCTCTCTCG 2132
Db      362 LysThrThrSerSerGlnLysGlnSerSerProGlnSerLeuProGlyAlaLeuGlyLeu 381
Qy      2133 GCTGTCGGGGGAGAGCG-----GAGGTCGGCTTGGCCAGGGG 2171
Db      382 SerValArgProLeuThrGlnGlnGlnLysSerPheAspValLysLeuGlyIleGly 401
Qy      2172 -----CCGAAATTTCCGCTGGGAGTGTGTGATCCATCCAG 2210
Db      402 LeuLeuValValSerValGluProAsnLysProAlaSerGluAlaGlyIle----- 418
Qy      2211 GTGCGGGGAGGAGCCCAACATCCCTTGAACAGATCTGTAAAGTCACTTCCAG 2270
Db      419 -----ArgGluGln-----AspIleIleLeu----- 425
Qy      2271 TTCTCCGATATTTCAAAACTGCTTCATGAGAGTCCCTCTCTCTAGCTTCCGCG 2330
Db      426 -----SerAlaAsnLeuLysProLeuGlnSerAlaAspAspLeuAlaAsnIle 441
Qy      2331 CTCTGC 2336
Db      442 IleCys 443

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RESULT 8
US-10-467-657-2096
/ Sequence 2096, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIANT Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ PRIOR FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqMan99, version 1.04
/ SEQ ID NO 2096
/ LENGTH: 499
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2096

Alignment Scores:
Pred. No.: 9,378-19 Length: 499
Score: 424.50 Matches: 135
Percent Similarity: 46.6% Conservative: 63
Best Local Similarity: 31.8% Mismatches: 137
Query Match: 7.6% Indels: 90
DB: Gaps: 14

US-10-617-443B-1 (1-3006) x US-10-467-657-2096 (1-499)
Qy      1083 GCTGACGTGTGGAGAGATGCGACCAACCGGTGTCAATAGACTTCTTCCGAGA--- 1139
Db      58 AlaGlnLeuValGlnSerGlnGlyProAlaValAlaAsnIleGlnAlaAlaProAlaPro 77
Qy      1139 ----- 1139
Db      78 ArgThrGlnAsnGlySerGlyAsnAlaGluThrAspSerAspProLeuAlaAspSerAsp 97
Qy      1140 -----CACCGCGTGTGGCGGCAACGTGCC--- 1166
Db      98 ProPheTyrGluPhePheLysArgLeuValProAsnMetProGlnIleProGlnGlnGln 117
Qy      1167 -----CTGTCCAGCGGTTCTGAGCTTCATCATGTCAGAGCGCGCTGATC 1211
Db      118 AlaAspAspGlyGlyLeuAsnPheGlySerGlyPheIleIleSerLysAsnGlyTyrIle 137
Qy      1212 ATCACCAGTGCACAGTGTGTCTCAGCAACAGTGTGCTCCCGGAGGAGGAGGAGCTCAG 1271
Db      138 LeuThrAsnThrHisValValAla-----GlyMetGlySerIleLys 151
Qy      1272 GTGCAAGCTTACAGATGGGAGCTCTCTAGAGCCACCATCAAGAAGATGACAGAAAGTGG 1331
Db      152 ValLeuLeuAsnAspLysArgGluTyrThrAlaLysLeuIleGlySerAspValGlnSer 171
Qy      1332 GACATTTGCCACCATCAAGATCCATCCCAAGAAAAGTCCCTGTGTTGCTGGAGTCAAC 1391
Db      172 AspValAlaLeuLeuLysIleAspAlaThrGlnGlnLeuProValValLysIleGlyAsn 191
Qy      1392 TCGGCGGACCTGGCGCTGGGAGATTGTGTGTCGTCATCGGAGTCCCTTGGCCCTACAG 1451
Db      192 ProLysAsnLeuLysProGlyGluTyrValAlaAlaIleGlyAlaProPheGlyPheAsp 211
Qy      1452 AACACAGTGAACACGGGATGTGTGACACTGCCCCAGCGGAGGAGGAGGAGTGGCGCTC 1511
Db      212 AsnSerValThrAlaGlyIleValSerAla-----LysGlyArgSerLeuPro--- 227
Qy      1512 CGGAGCTCCGACATGATGATCAACGAGGATGCGCATCATCACTACGAGAACTCCGGG 1571

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Db	228	hmgIuserTyTthrProheIIegInthrrarValAlAlaasnProGlyasnSerGly	247
Oy	1572	GGACCACTGGTGAACCTGGATGGCGAGGTCAATTGGCATCAACGCTCAAGTCAAG---	1622
Db	248	GlyProLeuPheAsnLeuGlySerGlnValValGlyIleAsnSerGlnIleTySerArg	267
Oy	1629	-----GCTGGCATCTCCCTTGGCAATCCCTCGAGCCGAGATCAACAGGTTCCTC	1678
Db	268	SerGlyGlyPheMetGlyIleSerPheAlaIleProIleAsp---ValAlaMetAsnVal	286
Oy	1677	ACAGAGTTCCAAAGACAGATCAAAAGACTGAAGAAGCCGTTCACTGGCATACGATG	1736
Db	287	AlaGln---GlnLeuLysAsnThrGlyLysValGlnArgGlyGlnLeuGlyAlaIleIle	305
Oy	1737	CGAGAGATCAACCAAGCTGGTGGATGAGCTGAAGGACGAAACCCGAGACTTCCCAAG	1799
Db	306	GlnGlnValSerTyGlyLeuAlaGlnSerPheGlyLeu-----Asp	319
Oy	1797	GTCAAGCATGGAATTATGTGCMAAGAGTTGGCCGCAATTCATCTTCCAGAGAGCGAG	1855
Db	320	LyvalAsnSerGlyAlaLeuIleAlaLysIleLeuProGlySerProAlaGlnArgIaGly	339
Oy	1857	ATCCAAAGTGGTGAATCATCTGTCAAGGTCAACGGGCGCTCTTAAGTGAATCTGAATGAG	1911
Db	340	LeuGlnAlaGlyAspIleValLeuSerLeuAspGlyGlyLuiAlaArgSerSerGlyAsp	359
Oy	1917	CTGCAGAGAGGCGGTG-----CTGACCCGAG-----TTCCTCTCTTACTAGAG	1955
Db	360	LeuProValMetValGlyAlaIleThrProGlyLysGlnValSer-LeuGlyValTTPArg	379
Oy	1959	GTGCGGCGGGGAGCAACGACCTCTCTTCAGCATGCGACCTGAAGGTGTCATGTAGGG	2018
Db	379	GlySerGlyGlnGluIleThrIleLysAlaLysLeuGlyAsn-----	392
Oy	2019	GCGCATTCCTCCAGGGCCCAAGGCTGCAGAGCTGCAGACAAGGAGGAGCGGCCCGG	2078
Db	393	-----AlaAlaGlnAsnThrGlyAlaSerSerTythrAspGlnAlaIleProTyThr	409
Oy	2079	AGATCAGAGACGAAGGACCAACCGTCCGATC-----CTCAGACGAGCGAGC	2122
Db	409	rgIuGlnGlnSerGlyThrPheSerValGlnSerAlaGlyIleThrGlnInThrHisThr	429
Oy	2121	AGCCCTCCCTCTGG-----CTGTCCGGGCGAGACGGAGGCTGG	2155
Db	429	TAspSerSerGlyLysHisLeuValValValArgValSerAspAlaAlaGlnArgAlaGly	449
Oy	2160	CTTGGCCAGGGAGC	2172
Db	449	ylLeuArgArgGly	453
RESULT 9			
US-10-454-437-56			
: Sequence 56, Application US/10454437			
: Publication No. US20050277115A1			
: GENERAL INFORMATION:			
: APPLICANT: Pompejus, Markus			
: APPLICANT: Koegele, Burkhard			
: APPLICANT: Schroeder, Hartwig			
: APPLICANT: Zelder, Oskar			
: APPLICANT: Haberhauer, Gregor			
: TITLE OF INVENTION: CORYNBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS			
: FILE REFERENCE: BGI-128PCN			
: CURRENT APPLICATION NUMBER: US/10/454,437			
: CURRENT FILING DATE: 2003-06-13			
: PRIOR APPLICATION NUMBER: US 60/141031			
: PRIOR FILING DATE: 1999-06-25			
: PRIOR APPLICATION NUMBER: DE 19931636.8			
: PRIOR FILING DATE: 1999-07-08			
: PRIOR APPLICATION NUMBER: DE 19932125.6			
: PRIOR FILING DATE: 1999-07-09			
: PRIOR APPLICATION NUMBER: DE 19932126.4			
: PRIOR FILING DATE: 1999-07-09			

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; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 199322920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO: 56
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-56

Alignment Scores:
Pred. No.: 1,67e-16 Length: 441
Score: 387.00 Matches: 127
Percent Similarity: 43.9% Conservative: 66
Best Local Similarity: 28.9% Mismatch: 128
Query Match: 6.9% Indels: 119
DB: 6 Gaps: 17

US-10-617-443B-1 (1-3006) x US-10-454-437-56 (1-441)
QY 794 AGCCGAGACGTGGAGCGCTTTTAACTTCCTCGG-----GTGAG 835
   |||::||: :: ||| |
Db 19 ThrProSerGIutrinAmsSerPheGLuHivValArgSerSerTyProGLnTrpLysAsn 38
      |||::||: ||| |
QY 836 CGAGGCCCTTCCCAATAGCCTGGTGATCATCTGCACACTGCTGTGTGGAGGGGTCCCACAG 895
   |||::||: ||| |
Db 39 ThrAlaSerAsnGlnAenPro-----TyProGly 48
      |||::||: ||| |
QY 896 GGCTCAGTGTCGTGGAGCTGTGCTGTGAACCTGGAGACAGGGGTCTCAGAGAAGGCTTCT 955
   :||::||: :||| |
Db 49 AlaGlyPheGlySerGluGlnAenThrLn-----GlnGlyAenGluGlnAlaLeuPro 66
      :||::||: :||| |
QY 956 CCTCTGCGCCACTGGGACATAGGCCTCTGGAGAGCTGGACAGATCGTGATCTCACATGATCA 1015
   ||||::||| |||||
Db 67 Ala-----TrpThr-----SerTrpAsnGlnProLeuSerThrAsp 79
      ||||::||| |||||
QY 1016 CCTGAGCCCTTCCCGCAGCGCAGG----- 1035
   |||::||: ||| |
Db 80 ValIysProAlaIySgLuLyArgLysValGlyIleGlyThrAlaLeuAlaLeuMetLeu 99
      |||::||: ||| |
QY 1039 ----- 1035
Db 100 ValGlySerIleAlaThrGlySerValValGlyAlaAlaIatThrGlnLeuGlySerAsp 119
   1040 ----TCTCCACAGGCT-----GAGCAGCGCGCGCTACAGATTCAACTTCATTGCTGA 108
      ||||::||| |||||
Db 120 SerSerThrProValAsnAlaLeuGluInProSerValGlnAlyThrThraSn-AlaGl 139
   1088 C-----GTGCTGGAGAMATCGACACAGCCGCTGTCTCAATAGACT 1125
      ||||::||| |||||
Db 139 uProGlySerAlaGluGlnAlaAlaIaValLeuProSerValValSerIleGlnAl 159
   1130 CTTCCTAGAGAACCCCGCTGTTGGCCGACAAGTCGCCCTGTCTCAGCGGTTCTGGCTTAAT 1168
      ||||::||| |||||
Db 159 alleThrArg-----ThrSerAlaSerGluGlySerGlySerIl 172
   1190 CATGTCAAGAGCCGAGCTGATCATCACCAATGCCCATGCTGTCTCAGACACAGTGTGC 1245
      ||||::||| |||||
Db 172 eileSerSerAspelyTyrrValmetThrAsnAhilvalValala----- 187
   1250 CCCGGGCGAGCAGCAG-----CTCAAGCTGCAAGTACAGAAATGGGGACTCCTATGA 1300
      ||||::||| |||||
Db 188 ----GlyIleGluInSerGlyValLeuGlnValSerPheSerAspGlyThrAlaGl 206
      ||||::||| |||||

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QY 1301 GGCCACCATCAGACATGACAGAGAGTCGACATTGGCCACCATGACATGATCCATCCAA 1360
    |||
Db 206 nlaaaphellleaaglyaspproserthrhaplilealvalillelyleryghapya 226
QY 1361 GAAAAAGCTCCCTGTTGTTCTGTCGGGTCACTCGCGCGACCTCGCGCCCTGGAGAGTTTGT 1420
    |||
Db 226 lseranleuprovalmetserphegilyaspserrhaplaleuglyvalglylnserva 246
QY 1421 GGTGGCCATCGGCAAGTCCCTTGCCCTACAGAAACACAGTGAACGGGCACTGTCAGCAC 1480
    |||
Db 246 lmetralvaliglyserproleuglyleuserserthrvalthrthglyllevalseral 266
QY 1481 TCCCCAGCGGAGGAGGAGGAGCTG-----GGCTCCGGGACTCCGACATGAGACTACAT 1534
    |||
Db 266 aValanhrpProvalargalaserglyaspglyglyluserserleuileapalal 286
QY 1535 CCAGACGATGCGCATCATCACTACCGGAACCTCGGGGAGCACTGCTGAACCTGGATGG 1594
    |||
Db 286 eglthrhaplalealileasnproglyasnserglyylproleuvalaspmehaspel 306
QY 1595 CGAGGTGATGGCATCAACACGCTCAAGCTC----- 1625
    |||
Db 306 yasnleuileglymetasnservalillealaserleserthrseraspserralagl 326
QY 1626 -ACGGCTGCATCTCTTTGGCATCCCTCCAGACGCGATCAGCGTTCTCAGACAGTT 1684
    |||
Db 326 yserileglyleuglypheaserleproserasn-----Phalalyahryva 342
QY 1685 CCAAGACAGACAGATCAAGACTGAGAG-----AAGCGCTTCATCGGATCGATGCG 1738
    |||
Db 342 lalalepgleuleileserthrlyglylnvalthrlnprometileglyvalglinvalol 362
QY 1739 GAGCATCACACCAAGCTGTGATGAGCTGAAGGCCAGCAACCGGACTTCCAGAGGT 1798
    |||
Db 362 ythr-----Asphanse 366
QY 1799 CAGCAGTGAATTATATGTCAGAGAGTTCGCCGAATTCACTTTCAGAGAGCGGCAAT 1858
    |||
Db 366 rValthrlyalavalillealaservalglinaspglyglylproalalaspaladlyle 386
QY 1859 CCAAGATGATGATCATCATCAAGCTCAAGCGGCTCTCTAGTGAAGTCAAGTGAAG 1916
    |||
Db 386 uclnproglyasplilevalthrlyleuasnmaparg---Valilleaspserrproasp 404

RESULT 10
US-11-074-176-4
; Sequence 4, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Kluenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altemann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Azcarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-4

Alignment Scores: 2,07e-13 Length: 423
Pred. No.: 335.50 Matches: 95
Score:

```

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Percent Similarity: 48.1% Conservative: 54
Best Local Similarity: 30.6% Mismatches: 114
Query Match: 6.0% Indels: 47
DB: 7 Gaps: 11

US-10-617-443B-1 (1-3006) x US-11-074-176-4 (1-423)

QY 1132 GGGCCCAACGTCCTCCCTGTCAGGGGTTCTGCTTCATCATGTCAGAGGCC----- 1202
    |||
Db 133 GlylybLeuglythrThyrserygluglyserSerValValTyrMetlyserenglylys 152
QY 1203 GGCCTGATCATCAACCAATGCCACCGTGTGTGTCACCAACAGTCTGCTCCCGGAGCGAG 1262
    |||
Db 153 GlyTyrIleValThrAsnashihvalilleserglyserAspala----- 167
QY 1263 CAGCTCAAGGTGACACTACAGATGGGACTCTCTATGAGGCCACCATCAAGATCAGC 1322
    |||
Db 168 --ValGlnValGlnLeuAlaasnlylystrValaserAlalyvalalglylybap 186
QY 1323 AAGAGTGGGACATTCGACCATCAACATCCATCCCAAGAAAAGCTCCCTGTTGTTG 1382
    |||
Db 187 SerThrThrAspLeuAlaValleuserlileapalalyryrValThrGlnThrIleaglu 206
QY 1383 CTGGGTCACTCGGCGGACCTGCGGCTGGGAGTTGTGTGTCATCGGCAAGTCCCTTC 1442
    |||
Db 207 RheglyaspserylserleuclnlaaglylnthrvalillealvalaglyserProleu 226
QY 1443 GCCCTACAG-----AACCACTGACAAACGGGATCTGTCAGACTGCCAGCGG----- 1490
    |||
Db 227 GlyserglyrlyalaserthrvalthrnglylileileseralaprohalargThrile 246
QY 1491 -----GAGGGAGGAGAGCTGGGCTCCGGGACTCCGACATGAGACTACATCAGAGG 1541
    |||
Db 247 SerThrSerSerglyasnlin-----GlnThrValilleglnthr 259
QY 1542 GATGCGCATCATCACTACCGGAACTCGGGGAGCACTGTGTAACCTGATGCGAGGATTC 1601
    |||
Db 260 Aspalalaleleasnproglyasnserglyglylaleuvalasnseralaglylnval 279
QY 1602 ATGGCATCAACACGCTCAAGCTC-----ACGGCTGCGATC 1637
    |||
Db 280 lileglylleasnsermetyleuvalaglnserSeraspglyThrserValgluglymet 299
QY 1638 TCCTTGGCATCCCTCGACCGGATCAGCGTTCCTCAGAGAGTTCAGAGCAAGCAG 1697
    |||
Db 300 GlypnealalleproserasnleuvalThrillealasnleu----- 315
QY 1698 ATCAAGACTGGAAG-----AAGCGCTTCATCGGATACGG-----ATGCGGAGG 1742
    |||
Db 316 Vallyblyblyllylthrargproglinleuglyvalargvalalaleuugly 335
QY 1743 ATCAACCAAGCTGTGATGAGTGAAGGCCAGCAACCGGACTTCCAGAGGTCAAC 1802
    |||
Db 336 lileproglualatryargSerargleuyllylser-----Asnleuyls 351
QY 1803 AGTGAATTATATGTCAGAGAGTTCGCCGAATTCACTTTCAGAGAGCGGCAATCCAA 1862
    |||
Db 352 SerglyllyllyrvalaleaserlleasnlyasnserSeralealalasnlaelymetlys 371
QY 1863 GATGATGATCATCATCAAGTCAAGCGGCTCTCTAGTGAAGTCAAGTGAAGTCAAG 1922
    |||
Db 372 Serglyaspseryllylthrlyvalaspglylyblyvalaspserylaleaserleuhs 391
QY 1923 GAGCGCTGTCAGCGAG-----TCTCTCTCTTACTGAGAGTGGCGGGGGGAAC 1973
    |||
Db 392 SerIleleuTyrSerHlalyvalaglyasprThrValasnleThrIleasnargasnly 411
QY 1974 GAGCACTCTCTTTCAGCATGCGCACTGAG 2003
    |||
Db 412 ArgaspsValasnleuylvalylsleuglu 421

RESULT 11
US-10-793-626-1824

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```

; Sequence 1824, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1824
; LENGTH: 317
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1824

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Alignment Scores:

```

Pred. No.: 2,29e-12 Length: 317
Score: 318.00 Matches: 86
Percent Similarity: 53.0% Conservative: 57
Best Local Similarity: 31.9% Mismatches: 79
Query Match: 5.7% Indels: 48
DB: Gaps: 11

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US-10-617-443b-1 (1-3006) x US-10-793-626-1824 (1-317)

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QY 1176 GGTTCGCTTCATC-----ATGTCAGAG---GCCGCGTCATCATCAACCAATGCCAC 1226
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 27 G|YserIyVallIeYrgInIIeserIglYserIaYrIleValItrrhaaenHs 46
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1227 GTGGTTCAGCAACAGTGTCTGCCCGGAGGAGCAAGTCAAGTGCAGTCAAGAAAT 1286
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 47 ValValAsp-----G|YAlaserIuIleYsValIglInleuHIsaen 60
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1287 GGGGACCTTCATGAGGCCACCATCAAGACATGACAGAAAGTCGACATTCGCCACATC 1346
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 61 SerIyegInValAspAlaYsLeuIIeGIYsAspAlaLeuHrAspIIeAlaVala 80
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1347 AAGATCCATCCCAAGAAAGCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1406
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 81 LyelIeYsAspHrIySgIYleYsAlaIIeGIInPheHIsaenSerIySValGIIn 100
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1407 CTTGGGAGTTTGTGTGTCATCGACAGTCCCTTGCCCTTACAG-----AACACAGTG 1460
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 101 ThIGlyAspSerValPheAlaMetGIYAsnProLeuGIYleuGIInPheAlaAsnSerVal 120
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1461 ACAAGCGGATCGTCAGCACTGCCAGCGGGAG---GCGAGGAGCTGGCGCTCCGGAGC 1517
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 121 ThIserIyIleIleSerIaSerGIuAygThrIleAspAlaenThrSerIaGIYAsn 140
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1518 TCCGACATGAGTATTCACAGAGATGCCATCATCAACGGAATCCGGGAGGAGCA 1577
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 141 ThrIyValaAsnValleuGIInThrAspAlaIaIleAsnProGIYsnerGIYsAla 160
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1578 CTGTGTAACCTGATGGCGAGGTGCATTTGGCATCAACAGCTCAAGTCAAGCT----- 1631
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 161 LeuValAspRIleAsnGIYsleuValaGIYIleAsnSerMetIyIleAlaIaIaGIIn 180
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1632 -----GGCATCTCTTTCGATCCCTTCAGACGCGATCACAGGTTCTCCACAGATTC 1685
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 181 ValIGIuGIYIleYIlePheAlaIleProSerAsnGIuValaYValIthrIle----- 197
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1686 CAAGACAGAGATCAAGACTGGAAG-----AAGCGCTTCATCGGATACGATGCGG 1739
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 198 ---GIuGIInleuValYsHIsGIYsIleGIuAygProSerIleGIYIleGIYleuIle 216
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 1740 AGCATCACACCAAGCCTGGTGTGATGAGTGAAGGCCAGCAACCCGGACTTCCAGAG-- 1796
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

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Db 217 AsnLeuSer-----GTCAAGCTGGAATTATGTCAAGAGTTGCGCG 1832
QY 1797 -----
Db 225 TyArgIyGIuIleuHIsrHrIleYsAspIySgIYValaIaIyVala----- 242
QY 1833 AATTCACCTTTCACAGAGCGGCATTCCAAGATGTGACATCATGTCAAGTCAACGGG 1892
Db 243 -----AspSerGIuAsnAlaIleYsGIYAspIleIleThrGIYleAspGIY 259
QY 1893 CGTCTCTAGTGAATCTGAGTGAAGTGCAG 1922
Db 260 LySgInIleYsAspAspHrAspIleuArg 269

RESULT 12
US-11-182-016-20
; Sequence 20, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 1717
; TYPE: PRF
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Grub
US-11-182-016-20

Alignment Scores:
Pred. No.: 8.27e-12 Length: 1717
Score: 309.50 Matches: 288
Percent Similarity: 29.7% Conservative: 73
Best Local Similarity: 23.7% Mismatches: 440
Query Match: 5.5% Indels: 417
DB: Gaps: 53

US-10-617-443b-1 (1-3006) x US-11-182-016-20 (1-1717)

QY 1 CAGGAGCTGGAAGTTTGAGTCTTCACACATCAAGTCCACAGATGTGTAGAGGGCAT 60
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 202 GIInGIYleu-----CyIeAspProIIeHIsrValaIaThr----- 213
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 61 ATTCAATCCCAATTTTTCAGATGAGAGATTGAGCCCAAGAAAGTAATCTGTCTGA 120
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 213 ----- 213
QY 121 GGCCACAGCTAGAAAGACAGCCAGCCGAA-----CCCTTG 162
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 214 -----ArgHIsGIInGIYProIIaAsnAygSerProGIYIYleuProThr 229
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 163 GTGTGTGAGCCCCCAGGCCAGTGTCTCATTTGCGGGGCTCGGAGGACAGGAGGCTG 222
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 230 ValCyAlaIeAspIleuTrAspSerIaIaIaIeGIY-----AlaHIsIleu 244
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 223 AGCAGATGTTTCCAG-----TGTGGGAATCGAGAGAGCCCGGAC 267
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 245 SerThrIleCyAlaGIInAygGIYProHIsGIYTrHrSerIaIyGIYTrHrAlaPro 264
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 268 AGCCCGTGCAGGAGACCCGAGGCTGTAGGCCCGCTGCACATGCTCTCAGGCTG 327
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 265 ArgHrIaIeAspIleuTrHrIleAspIleAspIleProSerIleAspIleGIYIleGIY 284
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
QY 328 -----TGTCTCGGAGCCACAGCCCTTACTGTCTGACG----- 360
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 285 ProGIuSerTrGIYTrPAlaGIInCyAspProCyAspGIYArgHrGIYArgValaCyGIYAla 304
    ||||| ||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||

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QY	361	GCAGAGAAATCTGAGCCCCGGGAAAGGCTCAAG-----GAACTCTGGAAACAACTCT	411
DB	305	ValArgGlyAarAlaAlaArgGluGluGluGluProGlnAlaGlyCyValGluLeuProArgPro-Ile	324
QY	412	AGCAAGTCGGGCTGGGGTGGTGGGSSCAAGTTAGACACAGATGTAGGGCCCTGTGGACTCAGA	471
DB	324	uGlnSerProArgGlyThrIleProGlnGlyValGTPArgGluGluGlyProProProGluThr	344
QY	472	AATTGGACAGCTCTTTGGCCCAAGAGGGGSCACGCTGTCTCCGGGCTGGGTAAGCTCAGAA	531
DB	344	rProGlyValAar--AlaProGluGlyPro-GlyAlaSerGlyProGly-----	359
QY	532	GGGTGACCTGGGGGGCTTCCATCAACCCCGGCTGGACACTGTGTAGTGGCCCAAGGCTC	591
DB	360	-----TrrSerThrProThrArgGluGluGlnIleAlaArgSerLeuProValSerP	377
QY	592	GGAGGACACAGCTGGAGCCCATAGAGAGAGGSCAGTTCTCTCTGTAAAGGTAATTGCTG	651
DB	377	roArgSerGlyCyAarPro-----ArgGlySerSerLeuGly-----GlyValAlaP	392
QY	652	TAGACATAGGG-----	662
DB	392	roSerArgGlyCyValArgSerLeuArgIleLeuProProGluAlaArgGlyAlaArg	412
QY	663	--AACAGACAGCCCAAGGCGGAGATTAACCCAGATCCAGCCCGGCTCACTCCCGTGG	720
DB	412	rGArgArgArgArgProGlyGluArgThr-----ThrTrrPyrProSerG	427
QY	721	GCTACGGGCATATTCCTTAACCTCTCTGTGAAGCTCTCTTCGACAGCTAGCAGAGGTCAGTG	780
DB	427	IuaSerArgGluArgGlySerGlnIleValysGlu-AlaSerCyS-----	439
QY	781	AGGGGGGTGAGAGGAGCCCAAGCACTGAGAAAGCCTTTTAACATTCCTGGGGTGAAGCAGC	840
DB	440	ArgSerArg-glySerProArgArgGly-----GlnCy	450
QY	841	CCCTTCCCAATGCTGTGTGTCACTGCACTGCTGTGTGTAAGGGGATCCCAAGGGGCTC	900
DB	450	spProThrGluProTrpGlyGln-----GlyArgCyGlnProProArgSe	465
QY	901	AGTGTGGCTAGAGCTGGCTGTGAATCTGGAGCAGGGGCTCAGAGAAAGCCTCCCTCC	960
DB	465	rProTrpIleSerAla-----LeuThrIleValIleGlnAlaSerAlaGlyMetProPro--	481
QY	961	TGCCCACTGGGAGATGAGGCTCTGGAGCTGGCAGAGCATGTGATCTCACTAGTGCACCTGG	1020
DB	482	-----GlyGlyGlyIleArgGluMetGluAlaArgIleAlaGlyIleAlaArg	495
QY	1021	CCCTTCCCGGCAAGGSCAGTGTCCACSCAGCTGAGAGCCCGGCTCAAGTTCAACTTCA	1080
DB	495	GAlaGlnAarSerAlaArgArg-----GlnArgAlaSerAlaIleAarSerLeuTr	510
QY	1081	TTGCTGAGCTGTGTGAGAAAGATCGACACAGCCGCTGTCCATTAAGCTCTTCCAGAC	1140
DB	510	PalArgArgArgArgGlyGluArgArgGlnArgAlaIleGlyAlaArg-----	525
QY	1141	AACCGGCTGTGG-----CCGCAAGCTGCCCTGTCCAGCGG-----	1177
DB	526	-ProAlaValIleGlyArgThrIleIleArgProArgArgProProValIleSerAenThrSe	545
QY	1177	-----	1177
DB	545	rAlaGlyAarCyValaGluArgGlyValGlnIleSerArgArgGlyProCySerSerIe	565
QY	1178	-----TTCTGGCTTCACTGTCAGAGCGG	1203
DB	565	uArgLeuSerProCySerSerLeuGlyLeuAarPoluIleTrpIleProIleIleProAarGlyArg	585
QY	1204	G-----CTGATCATATCA-----	1216
DB	585	GGLuGlyLeuProGluTrpAlaSerSerAlaAarIleArgProThrValProSerGlyAlaArg	605

QY	1217	CAATGGCCAAAGCTGGTGTCCGAGAAACAAGTGTCCCGGAGGAGGACAGAGCTGAGGTGC	1275
DB	605	oThLeuProArgHnIaLaGluHnIaSenSerLeuProProLeuThrAlaGln--Al	624
QY	1276	AGCTACAGAAATGGGGAACT-----CCTATGAGGCGCCACATCAAGAATCGACAAAG	1328
DB	624	asErThrAerThrGlyAlaValAlaArgProAlaGlyProSerSerGlyThrSerThrAlaSe	644
QY	1329	TCGGACA-----TTGCCACGATCAAGATTCATCCCAAGAAAAGCTTCCTGTGTG	1379
DB	644	rSerThnIaSerCyLeuGluProThrSerGlyLeuAlaArgSerSer-ProCySerA	664
QY	1380	TTTGTTGGGTCACTGGCGGCACTGGC-----GCCTGG-----GGAGTTTGTTGGTGCATC	1430
DB	664	IaAlaAlaAerSerHnIaSerProSerHnThrLeuThrIleSerGlyCyLeuAlaValAla	684
QY	1431	GGCAGTCCCTTCGCGCTACAGAAACAAGTGAACAAGCGGACATTCGTACAGACTGCCAAGCG	1490
DB	684	rgIuSer-----GluLys-SerGlyGlnAla	692
QY	1491	GAGGGCAAGGAGCTGGCGCTCCGGGAACTCGGACATGATCATCATCAAGCGATGCATC	1550
DB	693	ArgGlyAlaAlaValGlyValArg-----	700
QY	1551	ATCAACTACGGAACTCGGGGGACCACTGTGAACTGGATGGCGGAGTCATTGGCATC	1610
DB	701	-----ArgSerGlnGlyProLeuSerGlnSer-LeuGlyArg-----As	713
QY	1611	AACAGCGTCAAGGTCAAGCGGTGGCATCTCCTTTGCCA-----TCCCTTCAGACGCG	1661
DB	713	pThrProGlySerGlyValAlaMetSerProValProArgCyAlaGlyLeuGlyThrAl	733
QY	1662	ATCACAGCGTTCTCCACAGAGTTTCCAAAGACA--AGCAGATCAAGAATGGAGAGAGCG	1718
DB	733	agLynIaGlyAlaGlyLeuSerSerArgAlaArgGlyValArgGlyValSerGlyAenAlaG	753
QY	1719	TTTCACTGGCATACAGATGCGGAGCATACACAAAGCTGTGTGATGATGACTGAAGGC---	1774
DB	753	naIaerThAlaGluGlyAlaArgSer---ProAla-AerGlyThrAlaGluGlyTrpG	772
QY	1775	-----CAGCAACCGGAACTTCCAGAGGTG	1799
DB	772	lyGlyIaerProAerGlyAlaAlaLeuHnIaSerGlnGlnAlaGlyValProArg---P	791
QY	1800	AGCAGTGGAAATTTATGTGCAAGAGTTGCGCGGAATTCACCTTCTCGAAGAGCGGATC	1859
DB	791	roSerGlyThrValSerGlySerGly-----	799
QY	1860	CAAGATGTGATCATCATGTGTCAAGGTCAAGCGCGCTCTTAATGTGACTCGAGTGAAGCT-	1918
DB	800	-----ArgGlyHnIaSerProAlaCyValaProLeuGlnProAlaA	813
QY	1919	--GGAGAGGCGGTGTGACGAGTCTTCCT	1948
DB	813	rgAlaAlaAlaArgAlaAlaAlaValaProAlaAlaThrProAlaGlyValaAlaValAlaL	833
QY	1949	-----CCTATGAGAGTGTGGCGGGGAGAGACAGCACTCTCTTCAGACATCGACCTGAG	2003
DB	833	eugLyProAerGlyValAlaAlaGlyLeuValLeuCyGlyrAlaIaTrpGlyHnIaValaCyPr	853
QY	2004	GTGTGTCATGTGAGGGGCGCATTCCTCCAGCGCCCAAGCGTCAAGAGCTTCGACAAACGAG	2063
DB	853	roAlaGlyAerPrArgAlaAlaIaIaIaerProCySerPrHnAlaArgGlyProGlyAlaAerProIyProG	873
QY	2064	GGCAGCGCGCGCGGAGATCAAGCAAGGACGAC-----C	2099
DB	873	lyThrGlyValProGlySerGlyValGlyLeuCySerHnIaSerProGluGlyAlaGlyTrLeuT	893
QY	2100	GTGCGTCTCTCAAGACGCGGAGCGCTTCCTGGC-----TGTC	2138
DB	893	hrAlaAlaGlyAlaGlyValTrpProAerProAerGlyProAlaAlaIaThrAlaLeuLeuProA	913
QY	2139	CGGGGCAAGCGGAGGC-----TGGGCTTGGCGAGGGGCC	2174

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Db      913  lae|y|t|n|n|e|c|g|y|g|y|e|u|c|y|s|e|r|a|l|a|g|y|a|r|g|s|e|r|t|p|a|l|g|y|s|e|r|t|y|l|y|c 933
Qy      2175  g|a|a|t|t|c|c|g|c|t|g|g|g|a|g|t|t|g|-----g 2198
Db      933  y|v|a|l|a|g|y|c|y|e|r|h|c|g|y|p|r|o|l|a|a|l|a|g|y|p|r|o|a|r|g|a|l|a|g|n|c|y|a|r|g|h|i|s|e|u|p|r|o|g|y|a 953
Qy      2199  a|t|c|c|a|c|a|t|c|c|g|t|g|c|g|g|g|g|a|g|c|c|c|a|c|a|t|c|c|c|t|t|g|-----2242
Db      953  e|r|a|l|a|g|y|p|r|o|g|y|p|r|o|g|y|p|r|o|g|y|p|r|o|s|e|r|p|r|o|a|l|a|r|g|e|c|g|y|p|r|o|e|u|r 973
Qy      2243  -----a|c|a|g|a|t|g|a|t|c|t|-----g|a|a 2258
Db      973  r|o|g|y|p|r|o|e|u|r|p|r|o|a|r|g|a|l|a|g|y|u|g|l|u|e|r|p|r|o|a|l|a|t|h|r|p|r|o|g|y|a|r|g|y|g|l|y|u|p 993
Qy      2259  g|t|c|c|t|t|c|c|a|g|t|t|c|c|g|a|t|t|c|c|a|a|a|a|t|c|c|c|t|t|c|c|a|g|g|-----2306
Db      993  r|o|-----t|h|c|y|e|u|r|p|r|o|t|h|r|a|l|a|g|y|a|r|g|a|r|g|c|y|e|l|n|g|n|t|r|a|r|g|y|p|r|o|v|a|l|g|y 1012
Qy      2307  -----t|c|c|c|t|c|t|c|c|t|a|c|t|t|c|c|g|c|c|c|t|c|c|g|c|c|c|t|g|a|a|c|a|c 2348
Db      1013  a|l|a|r|o|g|n|p|r|o|e|u|a|l|a|g|n|p|r|o|g|n|l|e|u|e|u|a|l|a|p|r|o|g|n|n|p|r|o|t|r|p|a|l|a|t|h|r 1032
Qy      2349  c|a|t|t|g|c|a|g|a|t|c|c|c|t|c|c|t|c|c|c|t|c|c|a|c|a|g|t|t|g|g|c|t|g|c|c|a|a|g|t|t|c|t 2408
Db      1033  a|l|a|s|e|r|p|r|o|l|e|r|p|r|o|e|u|r|p|r|o|g|y|p|r|o|e|r|t|r|p|a|r|g|y|l|e|u|g|y|a|r|g|y|p|r|o|a|a 1052
Qy      2409  t|c|c|c|c|c|t|g|a|c|a|a|g|c|c|c|a|c|t|g|a|c|c|c|c|c|c|t|c|c|t|g|c|c|c|c|t|g|a|g|a|t|t|a 2468
Db      1053  g|l|y|s|e|r|a|r|g|s|e|r|a|r|g|y|g|l|n|a|l|a|-----p|r|o|l|y|s|e|r|c|y|a|l|a|r|p|r|o|a|r|p|r|o|g|y|l|n|a 1072
Qy      2469  c|c|a|a|-----g|c|t|g|a|g|c|c|a|g|g|c|t 2489
Db      1072  e|g|n|n|h|e|g|y|g|y|a|r|g|n|l|a|r|v|a|l|l|e|u|r|t|h|r|g|y|t|h|r|a|r|g|a|l|a|l|e|y|p|r|o|g|y|g|l 1092
Qy      2490  g|c|t|g|c|c|t|g|c|c|a|g|c|c|t|g|c|c|g|t|c|c|t|g|a|g|a|c|-----2520
Db      1092  y|a|l|a|r|g|a|r|g|t|h|r|e|u|l|y|s|e|r|a|r|g|a|r|g|p|r|o|e|r|p|g|y|a|l|e|g|n|a|l|a|r|v|h|i|s|e|l|n|c|y 1112
Qy      2521  -----a|g|n|c|a|t|g|-----2532
Db      1112  e|r|p|r|o|a|l|a|l|a|g|y|v|a|l|a|l|a|r|p|r|c|y|l|e|u|r|t|h|r|a|r|g|y|u|g|y|l|e|u|e|u|a|l|a|s|e 1132
Qy      2533  -----a|t|c|c|t|t|t|g|g|g|t|g|c|g|g|g|t|g|g|g|t|c|c|a|g|c|c|c|a|g|c|c|a|c|t|g|a|t|g|a|a|t|g|c|c 2588
Db      1132  r|a|l|a|t|h|r|p|r|o|-----t|r|p|a|l|a|l|a|r|p|a|l|a|t|h|s|e|r|g|y|h|i|s|e|l|n|c|y|c|y|s|e|r|p|r|o|g|y|u|c|y|e|r 1152
Qy      2589  c|c|t|g|c|c|t|g|c|c|a|g|c|t|g|a|g|c|c|c|c|c|c|t|g|c|c|a|t|g|a|g|t|t|t|c|c|c|c|c|a|g|c|c|a|g|c|a 2648
Db      1152  r|o|g|y|l|y|v|a|l|a|s|e|r|g|n|l|e|u|r|p|r|o|-----p|r|o|a|r|p|r|t|h|r|e|u|r|s|e|r|a|r|a|g 1166
Qy      2649  g|g|c|g|c|g|g|g|g|a|g|a|c|g|t|g|a|a|a|g|t|g|c|t|g|c|g|g|g|a|a|c|t|t|c|c|c|c|a|a|g|c 2708
Db      1166  l|y|a|l|a|s|e|r|g|y|l|e|u|r|g|h|i|s|p|r|o|r|p|r|o|t|h|r|h|i|s|t|r|p|g|y|l|e|u|r|p|r|o|s|e|r|p|r|o|a|r|g 1186
Qy      2709  g|g|c|c|a|-----t|g|g|g|g|c|a 2720
Db      1186  l|y|r|e|v|a|l|g|n|p|r|o|e|u|r|c|y|e|r|t|h|r|v|a|l|a|r|g|y|u|a|l|a|p|r|o|t|h|r|g|n|l|n|h|g|y|l|g|t|t|r|p|s|e|r|g 1206
Qy      2721  g|c|c|t|g|a|g|a|g|a|c|a|g|t|g|a|g|c|t|g|c|g|g|t|g|t|g|a|g|a|c|t|g|a|c|c|g|t|t|c|c|c|t|t 2780
Db      1206  l|y|c|y|v|a|l|a|g|n|s|e|r|t|e|u|y|g|l|n|g|y|l|e|u|h|i|s|e|l|y|t|r|p|r|o|e|u|r|p|r|o|a|r|p|r|o|s|e|r|p 1226
Qy      2781  c|c|c|a|c|c|a|g|c|t|t|g|g|a|t|g|c|a|g|c|c|g|c|t|c|g|a|t|g|a|g|t|g|c|c|g|c|c|c|a|g|a|g|c|a|t|g|c|a|g 2840
Db      1226  r|o|a|l|a|l|a|a|a|s|e|r|g|y|t|h|r|a|l|a|r|s|e|r|v|a|l|t|r|p|a|l|a|l|a|r|p|r|o|g|y|g|l|y|a|l|a|r|p|r|o|g|u|g 1246
Qy      2841  g|c|t|g|t|g|g|c|c|a|c|c|c|c|c|c|t|c|a|t|c|a|g|g 2869
Db      1246  l|y|s|e|r|t|r|p|a|l|a|l|a|g|n|p|h|e|v|a|l|p|r|o|g|y 1255
RESULT 13
US-11-186-284-33
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/ Sequence 33, Application US/11186284
/ Publication No. US20050266493A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Berger, Allison
/ APPLICANT: Guillemette, Tracy L.
/ APPLICANT: Kamackar, Shubhangi
/ APPLICANT: Schlegel, Robert
/ APPLICANT: Monahan, John E.
/ APPLICANT: Thibodeau, Stephen N.
/ APPLICANT: Burgart, Lawrence J.
/ TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
/ TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
/ FILE REFERENCE: MP001-0292P2RM
/ CURRENT APPLICATION NUMBER: US/11/186,284
/ PRIOR FILING DATE: 2005-07-21
/ PRIOR APPLICATION NUMBER: US/10/301,822
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 60/339,971
/ PRIOR FILING DATE: 2001-12-10
/ PRIOR APPLICATION NUMBER: US 60/361,978
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/381,988
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 228
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 33
/ LENGTH: 1466
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-11-186-284-33

Alignment Scores:
Pred. No.: 8 77e-12 Length: 1466
Score: 309.00 Matches: 238
Percent Similarity: 30.2% Conservative: 67
Best Local Similarity: 23.6% Mismatches: 362
Query Match: 5.5% Indels: 342
DB: 7 Gaps: 45

US-10-617-443B-1 (1-3006) x US-11-186-284-33 (1-1466)
Qy      139  c|a|g|c|a|g|c|c|c|c|c|c|c|c|c|c|t|g|t|g|t|g|t|g|c|a|g|c|c|c|c|c|c|c|a|g|t|t|g|t|c|t|a|t|t|g|c|g|g 198
Db      208  g|n|a|l|a|g|y|p|r|o|s|e|r|g|y|p|r|o|-----p|r|o|g|y|p|r|o|g|y|a|l|a|l|e|y|l 222
Qy      199  g|c|t|g|g|g|a|g|c|c|a|g|c|a|g|c|g|t|g|a|g|c|a|t|g|t|t|c|c|a|g|t|g|t|g|g|a|a|c|t|g|a|g|a 258
Db      223  p|r|o|s|e|r|g|y|p|r|o|a|l|g|y|l|y|s|-----a|s|p|g|y|c|l|u|s|e|r 233
Qy      259  g|c|c|c|g|-----c|a|c|a|g|c|c|c|g|t|g|c|a|g|g|a|a|c|c|c|c|a|g|g|c|t|g|a|g|c|c|c 303
Db      234  g|l|a|r|g|p|r|o|g|y|a|r|g|p|r|o|g|y|g|l|u|r|g|y|l|e|u|r|p|r|o|g|y|p|r|o|g|y|l|l|e|y|s|e|l|p|r|o 253
Qy      304  g|t|g|c|a|t|g|c|a|t|g|c|t|c|a|g|c|c|t|g|t|g|t|c|t|g|c|a|g|c|c|c|c|c|t|a|c|t|g|t|g|a|c|g|c|a 363
Db      254  -----a|l|e|g|y|l|e|r|p|r|o|g|y|l|h|e|-----p|r|o|g|y|e|l|y|s|e|l|h|i|s 265
Qy      364  g|c|a|g|a|a|t|c|t|g|a|c|c|c|g|a|a|g|t|c|c|a|g|-----g|a|a|g|t|c|t|g|a|a|c|a|t|t|a|g|c|a|g|t|c|g 420
Db      266  a|r|g|y|p|h|e|r|p|g|y|a|r|g|a|n|g|y|g|l|u|y|s|e|l|g|y|t|h|r|g|y|a|l|a|p|r|o|g|y|l|e|u|l|y|s|e|l 285
Qy      421  g|c|t|g|g|g|t|g|t|g|g|c|c|a|a|t|t|a|g|c|a|c|a|g|a|t|t|a|g|g|c|c|c|t|t|g|a|c|t|a|g|a|a|t|t|g|g|a|g 480
Db      286  g|l|u|a|n|g|y|l|e|u|r|p|r|o|g|y|g|l|u|a|n|g|y|a|l|a|r|p|r|o|g|y|p|r|o|e|r|g|y|-----300
Qy      481  c|t|c|t|t|t|g|c|c|c|a|g|a|g|g|c|c|a|c|g|t|g|t|g|t|c|c|g|g|c|c|t|g|g|t|a|c|t|c|a|g|a|g|g|t|c|a|c|c|t 540
Db      301  -----p|r|o|a|r|g|y|a|l|a|-----p|r|o|g|y|g|l|u|r|g|y|a|r|g|p|r|o|g|y|l|e|u|r|p|r|o 314
Qy      541  g|g|-----g|g|t|t|t|c|c|a|c|t|a|c|a|c 558
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Db 315 GIYAlaAlaGlyAlaArgGlyAaAaAaGlyAlaArgGlySerAaAaGlyGlnProGlyPro 334
 QY 559 CCCCGCTGAGACAGCTGCTAGCCCGAGGGCTCGAGAGGACCAAGCTGGAGCCCATAGAGA 618
 Db 335 ProGlyL-----ProProGlyThraAlaGlyPheProGlySerProGlyAlaA 349
 QY 619 GAGGCGAAGTTCTCTCTGTAAGGGATATGCTGTAGCATGAGGAGAAACAACAAGGCCAG 678
 Db 350 LybGlyGlnValGlyProAlaGly-----SerProGlySerAaAaGlyAlaPro 365
 QY 679 GGGGACATACCCGAGATCCAGCCCGCCCTCACTCCGCTGAGCTTCACGCAATATCTCA 738
 Db 366 GlyGlnArgGlyGlyLuproGlyProGlnGlyHis----- 376
 QY 739 ACCTCTCTGAGCCCTCTGCGCCAGCTTACAGGCTTCAGTGAAGGGGGTGAAGAGCC 798
 Db 377 -----AlaGlyAlaGlnGlyProProGlyProProGlyAlaAaAaGlySerPro 392
 QY 799 AGCAGGTGAGACCTTTTAACCATTTCTCGGGGTGAGAGCCCGCTTCCCAATGAGCTG 858
 Db 392 oGlyL-----GlyLybGlyGlnMetGlyProAlaGlyAlaProGly 405
 QY 859 TGTCACTGACCTGCTGTGTGTAGGGG-----TCCCAACGGGCTCACTGTGGCTGA 912
 Db 405 YAlaProGlyLeuMetGlyAlaArgGlyProProGlyProAlaGlyAlaAaAaGlyAlaPro 425
 QY 913 G-----GCTGGCTCTGACTGGAGACAGGGGCTCTCAAGAAAGACCTCTCTC 957
 Db 425 oGlyLeuAaArgGlyGlyAlaGlyGlyLuproGlyLybAaAaGlyAlaLybGlyLuproGlyPro 445
 QY 958 TCTCTGCGCCAGTGGGACATAGGCC----- 979
 Db 445 oArgGlyGlyLuproGlyGlyAlaGlyAlaGlyAlaProGlyAlaLybGlyGlyLuproGly 465
 QY 980 -----TCTGGAGCTGGACAGCATCTGATCTCACTGATGACAGCTGGCTTCCCGAGCG 1035
 Db 465 YLybAaAaGlySerProGlyGlyLuproGlyAlaAaAaGlyLeuProGlyAlaAlaGlyGlyLup 485
 QY 1036 CAGGCTCTCAACAGCTGAGACAGCCCGCTCAACAGTTCAATTCATTCGTCAGTGT-- 1093
 Db 485 GgLyAlaAaProGlyPheAaArgGlyProAlaGlyProAaAaGlyAlaProGlyGlyLybGlyPro 505
 QY 1094 -GGAGAAGATCGACAGCCGAGCTGTCACATAGAGCTTCCGAGAGACCCGCTGTTG 1152
 Db 505 oAlaGlyGlyLuproGlyAlaProGlyPro-----AlaGlyProAaGlyAlaAla----- 521
 QY 1153 GCCGCAACGTGGCCCTGTCTCAGCGGTTCTGGCTTCATCTCAAGAGCGCGGCTGATCA 1212
 Db 522 -----GlyGlyLuproGlyAa 526
 QY 1213 TCACCAATGCCAAGTGTGTCTCAGCAACAGTGTGCTCCCGGAGAGGACAGCTCAAG 1272
 Db 526 GAaAaGlyAlaProGlyGlyProGlyLuproGlyLuproGlyLuproGlySerProGly-----G 544
 QY 1273 TGCAGTACAGAGAGGGGAGCTCTTGAAGAGCCACATCAAGAGCATCAAGAAAGTGG 1332
 Db 544 YProGlySerAaP--GlyLybAaPro--GlyProProGlySerGlnGlyLuproGlyAaG 562
 QY 1333 ACATTCGCAACATCAAGATTCATCCCAAGAAAGAGCTCTGTGTGTGTCT----- 1384
 Db 563 ProGlyProProGlyProSerGlyProAaGlyGln--ProGlyAlaMetGlyPheProGly 582
 QY 1385 -----GGGTCACTCGGCGGAGCTGGCGGCTGGGAGCTTGTGTGTGCA 1428
 Db 582 YProLybGlyAaAaAaGlyAlaProGlyLybAaAaGlyGlyAaGlyGlyProGlyGlyPro 602
 QY 1429 TCGGAGAGTCCCTTCGCTCAAGAAACAGTGAACAGGAGCATCG-----CA 1476
 Db 602 oGlyProGlnGlyProProGlyLybAaAaGlyGlyLuproGlyProGlnGlyProProGlyPro 622
 QY 1477 GCATTCGCGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1533
 Db 622 oThrGlyProGlyGlyAlaAaAaGlyLybAaAaGlyProProGlyPro----- 636

QY 1534 TCCAGACGAGTGCATCATCACTACGGAAGCTCCGGGGAGCACTGTGAAGCTGTGAG 1593
 Db 637 -ProGlnGly-----LeuGlnGlyLeuProGlyLuproGlyProProGlyGly 652
 QY 1594 GCGAGGTCAATTGGCATCAACAGCTCAAGGTCAAGGCTGGCATCTCTTGTGCATCCCT 1653
 Db 652 uAaAaGly----- 654
 QY 1654 CAGACCGCATCAACAGGTTCTCACAAGATTCCAAGAGATCAAGAGATCAAGAGACTGGA 1713
 Db 654 ----- 654
 QY 1714 AGCGTTCAATGGCATAGGAGTGGAGATCAACAGCTGTGATGAGCTGAAG 1773
 Db 655 -----LybProGly----- 657
 QY 1774 CCAGAACCCGAGACTTCCAGAGTCAAGATGGAATTTATGTGCAAGAGTTGCGCGCA 1833
 Db 658 -----GluProGly-----ProLybGly----- 663
 QY 1834 ATTCACTTCTCAGAGAGGCGGATCAAGATGTGATCATCTGTCAAGGTCAACGGGC 1893
 Db 663 ----- 663
 QY 1894 GTCTCTAGTGAAGTCAAGTGAAGTCAAGAGGCGGCTGACCGAGTCTCTCTCTAC 1953
 Db 664 -----AaAaAaGlyAlaProGlyAlaProGlyAlaLybAaAa----- 676
 QY 1954 TGAAGTGTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2013
 Db 677 -AlaGlyAlaProGlyGlyLuproGlyPro----- 686
 QY 2014 GAGGGGCGCATTCCTCAAGCGGCAAGCTCAAGCTGCAACAGAGGAGGAGGAGGAGGAGGAG 2073
 Db 687 -----GlyLeuAlaGlyAlaProGlyLeuAaGlyAlaGlyAla 700
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 Db 700 oPro-----GlyProGlnGlyLybGlyAlaAaGlyProProGlyProProGly 717
 QY 2134 CTGTCCGGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2193
 Db 717 YAlaAlaGlyLuproGlyLuproGlyLuproGlyLuproGlyLuproGlyLuproGlyLupro 734
 QY 2194 GTTGAATCAATCCCGGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2253
 Db 734 uGlySerProGlyProLybGlyAaAaGlyGlyLuproGlyGlyProGlyAlaAaAaGly-- 753
 QY 2254 TGAAGTCACTTCCAAAGTTCTCCGATATTCACAAAGCTCTTCATGAGAGGTCCCTC 2313
 Db 754 -----ValProGlyLybAaAaGlyProAa 761
 QY 2314 CTCTCTAGC-----TTCGCGCTCTGCGCTGTGAACACCATCTGAGATCTCC 2364
 Db 761 GgLyProAaAaGlyProGlyLuproGlyProGlyProGlyProGlyProGlyProGlyProGly 781
 QY 2365 CTGTCTGCGCT 2424
 Db 781 LuGlyGlyAlaProGlyLeuProGlyAlaGlyProAaGlyLuproGlyLuproGlyLuproGly 801
 QY 2425 CCCACTGACCTGAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2483
 Db 801 LyGlnThr-----GlyPro-----ProGlyProAlaGlyPheProGlyAlaProGly 817
 QY 2484 -----AGGCTGTGCTCT 2496
 Db 817 LuAaGlyLuproGlyGlyLybGlyLuproGlyAlaProGlyLuproGlyLuproGlyLuproGly 837
 QY 2497 GCCAGCTGGAGTCT-----CTGAGAGACAGTCACTCATCTCTCTCTCTCTCTCTCTCTCTCT 2547
 Db 837 LyProProGlyAlaAlaGlyProProGlyGlySerGlyProAlaGlyProProGlyProGly 857

[illegible]

Db	764	gglYprOthrhglYprOllleglYprOprO-glyPrOalaelYglNprOglYaelYglYg	764
Qy	2365	CTGCCTCTGCCCCCTCTACTGACAGCTTGAGGCTGCCAACCTTCTTCCCTGACAAAG	242
Db	764	lUglYglYAlarProglYleuPrOglYlIlealaglyPrOarnglYserPrOglYgluarG	804
Qy	2425	CCCACTGAACCTAGAGCCGCCAGCTTCCCTCTGCCCCCTTACCAAGCTGAGGGCCA	248
Db	804	YglUthr-----glYprO-----PrOglYPrOalaglyPheprO-----	815
Qy	2485	GAGCTGCTGCTGCCCCAGCCAGCTGGGGTCCCTGGAGAGACAGTCAATCATCTGATCCCTTGGGG	254
Db	816	--glYAlarProglYglNleaglYglNPrOglYglYluelYglUaaglyAlarProglYg	835
Qy	2545	TGCGGGGGTGGGT-----CCAGCCCAAGAGCAGGCACATGAATGAATGCCCT-----	259
Db	835	lulYglYglUglYglYglYprOprOglYAl-alagly-----PrOprOglYlye	850
Qy	2593	--GGCTGGAGACTGAAGCCCCGCCCTGCACATGAGTTTCTCCCCAGGACGACAGAG	264
Db	851	AarglYthrserylYhIsPrOglYprOllleglYprOprOglY-PrOarnglyAaArngl	870
Qy	2650	GCGCGGGGAGACAGCTGGAATTTGGCTGCTGCTGCGGGAGACTTCTCT-----CCCC	270
Db	870	YglUarnglYserglYglYserPrOglYhIa-PrOglYglNPrOglYprOprOglYprO	890
Qy	2704	AAGCGGCATGGGCGACGCTGACAGCA	2732
Db	890	roglYAlarProglYprOprOglYglY	899
RESULT 15			
US-11-182-016-23			
; Sequence 23, Application US/11182016			
; Publication No. US20060019294A1			
; GENERAL INFORMATION:			
; APPLICANT: SOGEN, INC.			
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS			
; FILE REFERENCE: 038602/0102			
; CURRENT APPLICATION NUMBER: US/11/182, 016			
; CURRENT FILING DATE: 2005-07-15			
; PRIOR APPLICATION NUMBER: US/09/958, 359			
; PRIOR FILING DATE: 2002-02-05			
; NUMBER OF SEQ ID NOS: 55			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 23			
; LENGTH: 1742			
; TYPE: PRT			
; ORGANISM: Unknown Organism			
; FEATURE:			
; OTHER INFORMATION: Description of Unknown Organism: Grub			
US-11-182-016-23			
Alignment Scores:			
Pred. No.: 6,936-10 Length: 1742			
Score: 277.50 Matches: 273			
Percent Similarity: 33.3% Conservative: 113			
Best Local Similarity: 23.5% Mismatches: 426			
Query Match: 5.0% Indels: 349			
DB: 7 Gaps: 62			
US-10-617-443B-1 (1-3006) x US-11-182-016-23 (1-1742)			
Qy	24	TCACAACATCGATTCCCAACAGATGTGTGT-----AGSAGGACATATTCAGTCCCATTTTTCAGA	80
Db	396	SerleuLeuAenArAaYArGArGYSerlyAaYglYrThnTrPrArGrhIaPhePheArG	415
Qy	81	-----TGAGGAGTTGAGGCCCCAGAGAACTGAAGTATCTGTCTGAGG---CCACACAGC	131
Db	416	ProglNmetThrVallyglYserYrG-----CyelYserCyPPrOcyPser	431
Qy	132	TAGAAAGCAGCCAGGCCACCCAGAACCCCTGTGTGTGTGACG-----CCCAAGCCC	182
Db	432	PheArGSerlIeSerGlNprOgrYhIaSerThrAlaSerArYserleuPrOarGAla	451

Db 1382 ArgGlyProArgProPheTrpCysAlaLeuArgCysLeuArgTrpArgPro 1399

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 21, 2006, 21:02:06 ; Search time 47 Seconds
(without alignments)
587.525 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679

Sequence: 1 MHLLPASAGLHQLSSPRK.....LEVRGNDLLFSLAPEVVM 334

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
 - 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/ECTUS_COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1034.5	61.6	323	US-09-949-016-10514	Sequence 10514, A
2	1034.5	61.6	447	US-10-104-047-2765	Sequence 2765, Ap
3	1034.5	61.6	480	US-09-949-016-6270	Sequence 6270, Ap
4	1027.5	61.2	480	US-08-923-454A-18	Sequence 18, Appl
5	882	52.5	458	US-08-923-454A-8	Sequence 8, Appl
6	882	52.5	458	US-08-923-454A-25	Sequence 25, Appl
7	882	52.5	458	US-09-008-271A-11	Sequence 11, Appl
8	882	52.5	458	US-09-968-415-11	Sequence 11, Appl
9	882	52.5	529	US-09-075-460-5	Sequence 5, Appl
10	878	52.3	458	US-08-923-454A-31	Sequence 31, Appl
11	862.5	51.4	400	US-09-724-864-55	Sequence 55, Appl
12	779	46.4	423	US-08-923-454A-6	Sequence 6, Appl
13	779	46.4	436	US-08-923-454A-29	Sequence 29, Appl
14	564	33.6	323	US-08-923-454A-4	Sequence 4, Appl
15	564	33.6	377	US-08-923-454A-27	Sequence 27, Appl
16	454	27.0	491	US-09-438-185A-980	Sequence 980, App
17	450.5	26.8	474	US-09-489-039A-13694	Sequence 13694, A
18	441.5	26.3	455	US-09-711-164-416	Sequence 416, App
19	431	25.7	355	US-09-711-164-417	Sequence 417, App
20	428	25.5	460	US-09-199-637A-132	Sequence 132, App
21	425	25.3	475	US-09-252-991A-29494	Sequence 29494, A
22	424	25.3	173	US-08-923-454A-2	Sequence 2, Appl
23	422	25.1	475	US-08-350-741-2	Sequence 2, Appl
24	422	25.1	475	US-08-463-875A-2	Sequence 2, Appl
25	418	24.9	475	US-08-278-091-6	Sequence 6, Appl
26	418	24.9	475	US-08-483-859-6	Sequence 6, Appl
27	418	24.9	475	US-08-472-173-6	Sequence 6, Appl

28	418	24.9	475	1	US-08-487-167-6	Sequence 6, Appl
29	418	24.9	475	1	US-08-482-816-6	Sequence 6, Appl
30	418	24.9	475	1	US-08-296-149-6	Sequence 6, Appl
31	418	24.9	475	1	US-08-801-459-6	Sequence 6, Appl
32	418	24.9	475	1	US-08-615-271-6	Sequence 6, Appl
33	418	24.9	475	2	US-09-074-660-6	Sequence 6, Appl
34	418	24.9	475	2	US-09-074-659-6	Sequence 6, Appl
35	418	24.9	475	2	US-09-106-468-6	Sequence 6, Appl
36	418	24.9	475	2	US-09-106-466A-6	Sequence 6, Appl
37	418	24.9	475	2	US-09-106-467-6	Sequence 6, Appl
38	418	24.9	499	2	US-09-673-898-6	Sequence 6, Appl
39	417	24.8	360	2	US-09-489-039A-13634	Sequence 13634, A
40	415.5	24.7	409	2	US-09-902-540-11885	Sequence 11885, A
41	415	24.7	370	2	US-09-673-898-8	Sequence 8, Appl
42	414	24.7	414	2	US-09-388-090-6	Sequence 8, Appl
43	414	24.7	463	1	US-08-485-569-2	Sequence 2, Appl
44	414	24.7	463	1	US-08-480-993-2	Sequence 2, Appl
45	414	24.7	463	1	US-07-903-079B-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-949-016-10514
; Sequence 10514, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10514
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10514

Query Match
Best Local Similarity 61.6%; Score 1034.5; DB 2; Length 323;
Matches 203; Conservative 60; Mismatches 35; Indels 9; Gaps 2;

QY 10 GHHQSLSPRYKFNFIADYVEKIPAVVHIEFLRHLPRGRNVPLSSGSGFIMSEAGLIIT 69
DB 1 GQEDNSLSRHKNFPIADYVEKIPAVVHIEFLRKLPSKREVPVSSGSGFIVSEGLIYT 60
QY 70 NAAVTSNSAAPRQOQLKVOLONGDSYRATIKDIDKSDIATIKHPKKKPVLLHGSA 129
DB 61 NAAVVTN-----KRVAVELKNGATYEAKIKDVEKDIALLIKIDHOGKPVLLHGSS 114
QY 130 DLRPGEFVAIGSPALONTVTTGIVSTAOREGRELGRDSMDVYIOTDAIINYNSGCP 189
DB 115 ELRPEFVAIGSPSPSLONTVTTGIVSTOEGKELGRNSDMYIOTDAIINYNSGCP 174
QY 190 LVNLDEGVIIGINTLKVTAAGISFAIPSDRITFLTEFODKQIKD--WKRFIGIMRTIT 246
DB 175 LVNLDEGVIIGINTLKVTAAGISFAIPSDRITFLTEFODKQIKD--WKRFIGIMRTIT 234
QY 247 PSVLDELKASNPDPPEVSSGIYQEVAVNSQKQIGDSDIIVVNGRPLVDSSELQEA 306
DB 235 SSKAKELDRDRDPDVIISGAVIIEVPTDAEAGLKENYVVISINOQSVSANDVDV 294
QY 307 VLTSPLLLLEVRGNDLLFSLAPEV 333
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TELEX:
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-923-454A-18
Feature - 213 Gly/val polymorph

Query Match 61.2%; Score 1027.5; DB 2; Length 480;
Best Local Similarity 61.8%; Pred. No. 6.5e-102;
Matches 202; Conservative 60; Mismatches 56; Indels 9; Gaps 2;

10 GLHQLSPRYKFNFIADVVEKIAPAVNHTELFLRHPLEFRANVPLSSGSGFIMSEAGLIIT 69
158 GQEDNSLRHKTNFIADVVEKIAPAVNHTELFRKLPFSKREVPVSSGSGFIVSEDXLIVT 217
70 NAAVVSNSAAPRQOLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHS 129
218 NAAVVTN-----KRAVKVELKNGATYEAKIKDVEKADIALIKIDHCKLPVLLGHS 271
130 DIRPEEFVAIGSPALQNTVTGIVSTRQREGRELGRDSDMDYIQTDAIINYNGSGGP 189
272 ELRPEEFVAIGSPALQNTVTGIVSTRQREGRELGRDSDMDYIQTDAIINYNGSGGP 331
190 LVNLGEGYIGINTLVKTAGISPAISDRITRFLTEFQKQID---WKRRFGIMRTIT 246
332 LVNLGEGYIGINTLVKTAGISPAISDRITRFLTEFQKQID---WKRRFGIMRTIT 391
247 PSVLDELKASNDPFEVSSGIYQVAPNSPQSGGIQDGDIIYKNGRPLVDSSELOBA 306
392 SSKAKELDRHRDPDIVSGAYIIIEVPTPAAGLAKENDVIISINGSVSANDVSDV 451
307 VLTESPILLEVRGNDLLFSIAPREV 333
452 IKREBTLNMMVVRGNDIMITIVIPREI 478

RESULT 5
US-08-923-454A-8
Sequence 8, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Liyi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkebeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-923-454A-8

Query Match 52.5%; Score 882; DB 2; Length 458;
Best Local Similarity 52.5%; Pred. No. 3.1e-86;
Matches 169; Conservative 72; Mismatches 71; Indels 10; Gaps 2;

15 SSPRYKFNFIADVVEKIAPAVNHTELFLRHPLEFRANVPLSSGSGFIMSEAGLIITNAHV 74
141 ASPRQYNFIVADVVEKIAPAVNHTELFLRHPLEFRANVPLSSGSGFIVSEDXLIVTNAHV 200
75 SSNSAAPRQOLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSADLRG 134
201 AD-----RRRYRRLISGDIYEAADVAVDPAVADIAIRIQTEPLPTLPERSADVQSG 254
135 EFVVAIGSPALQNTVTGIVSTRQREGRELGRDSDMDYIQTDAIINYNGSGGPLVND 194
255 EFVVAIGSPALQNTVTGIVSTRQREGRELGRDSDMDYIQTDAIINYNGSGGPLVND 314
195 GEVIGINTLVKTAGISPAISDRITRFLTEFQKQID---IKWKRRFGIMRTITPSLV 250
315 GEVIGINTLVKTAGISPAISDRITRFLTEFQKQID---IKWKRRFGIMRTITPSLV 374
251 DELKASNDPFEVSSGIYQVAPNSPQSGGIQDGDIIYKNGRPLVDSSELOAVL 310
375 AELQREPSFPDVQGVLIHKVILGSPHARGLRPGDVILAIGEQVQNAEDVYEAVRTQ 434
311 SPILLEVRGNDLLFSIAPREV 332
435 SOLAVQIRRGRETLTVYTPREV 456

RESULT 6
US-08-923-454A-25
Sequence 25, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Liyi, George
APPLICANT: Kairan, Eric
APPLICANT: Clinkebeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406


```

Db      435 SQLAVQIRGRGRTLLTYTPREV 456

RESULT 9..
US-09-075-460-5
; Sequence 5, Application US/09075460A
; Patent No. 6489136
; GENERAL INFORMATION:
; APPLICANT: Zeytob, Antonio S
; TITLE OF INVENTION: CELL PROLIFERATION RELATED GENES
; FILE REFERENCE: 10284/004001
; CURRENT APPLICATION NUMBER: US/09/075, 460A
; CURRENT FILING DATE: 1998-05-08
; EARLIER APPLICATION NUMBER: US 60/046,077
; EARLIER FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 529
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-075-460-5

Query Match      52.5%; Score 882; DB 2; Length 529;
Best Local Similarity 52.5%; Pred. No. 4e-86;
Matches 169; Conservative 72; Mismatches 71; Indels 10; Gaps 2

Qy      15 SSPRYKFNFIADVVEKIAPAVVAHIELFLRHPFLGRNVPLSGSGGFIMSEAGLIITNAHV 74
      ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      212 ASPRSQVNFIDVVEKTAFAVVYIEILDRHPFLGRREVDSINSQGFVAVADGLITNAHV 271
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      75 SSNSAAPGRQOLKYLQLONGDSYEATKIDDKSDIATIKHPKKGLPVULLGHSADLRG 134
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      272 AD-----RRRVRLLSGDTYEAVVAADVADVADATLRIGTKBPLPLGRSADVROG 325
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      135 EFVAIGSPFLQNTVTGTGIYSTQREGRELGRSDSDYIOTDAIINYGNSGCPVLND 194
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      326 EFVAWMSGFLQNTITTSIGVSSAQRPARDLGLPTNVEYIOTDAIDFGNSGCPVLND 385
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      195 GEGVINTLKTAGISFAPISPSDRIITFLTEPODKQ----IDMKKRFTGIRMRITTPSLV 250
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      386 GEGVINTMTKTAGISFAPISPSDRIITFLTEPODKQ----IDMKKRFTGIRMRITTPSLV 445
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      251 DELKASNDPFPEVSSGIYQVAPNPSQRCGIGDGLIIVKNGRPLVDSSELQAVLTE 310
      :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      446 AELQREPSFDVQHGVLHKVILIGSPHARAGLRPGVITLAIIGEOMVNAEDVEAVRQ 505
      :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy      311 SPILLEVRGNDLLFSIAPREV 332
      ||:|||||:|||||:|||||
Db      506 SQLAVQIRGRGRTLLTYTPREV 527
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RESULT 10
US-08-923-454A-31
; Sequence 31, Application US/08923454A
; Patent No. 6004794
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caretha
; APPLICANT: Livl, George
; APPLICANT: Kattan, Eric
; APPLICANT: Clindenbeard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORIGINAL SOURCE: 24 Xaa = Arg or Cys
; ORIGINAL SOURCE: 278 Xaa = Ala or Val
US-08-923-454A-31

Query Match      52.3%; Score 878; DB 2; Length 458;
Best Local Similarity 52.2%; Pred. No. 8.5e-86;
Matches 168; Conservative 72; Mismatches 72; Indels 10; Gaps 2;

15 SSPRYFNFADVVEKIAVAVHIEFLRHPVLRGVRVPLSSGSGFIMSEAGLITNAHV 74
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Db 141 ASRSQYNFADVVEKIAVAVHIEFLRHPVLRGVRVPLSSGSGFIMSEAGLITNAHV 200
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 75 SSNSAAGRQQLKVOLONGDSYEATIKDIDKSDIATIKIHPKKLPVLLGHSADLRG 134
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 201 AD-----RRVAVRLSGDTYEAVVAVDVPADVADITLRIGTEPEPLPLGMSADVRG 254
   :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 135 EFVVAIGSPALONTTGTGIVTAOREGELGIRDSDMDYTQDAIINTGNSGGLVND 194
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 255 EFVVAIGSPALONTTGTGIVTAOREGELGIRDSDMDYTQDAIINTGNSGGLVND 314
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 195 GEVIGINTLKVTAIGISFPAISDRITRFLTEFODKQ----IKMKKRFIGIRKRTTPSLV 250
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 315 GEVIGINTLKVTAIGISFPAISDRITRFLTEFODKQ----IKMKKRFIGIRKRTTPSLV 374
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 251 DELKASNPDPPEVSSGIYQEVAPNSPSQGGIQQDDGIYKNGRPLVDSSELOEAVLTE 310
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 375 AELQAREPSPDYQVGHVLIHKVILGSPARAGLRPGDVILALGEGVQVAEDYEAVRTQ 434
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 311 SPILLEVRGNDLLFSINPEV 332
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Db 435 SOLAVQIRGRGRTLLVTPPEV 456
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RESULT 11
US-09-724-864-55
; Sequence 55, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Muriel, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.105001
```

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; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-55

Query Match      51.4%; Score 862.5; DB 2; Length 400;
Best Local Similarity 57.2%; Pred. No. 3.2e-84;
Matches 167; Conservative 61; Mismatches 53; Indels 9; Gaps 2;

QY 45 PLFGNVPSSGSGFIMSEAGLITNAHVSNASAPRQQLKVOLONGDSYEATIKDID 104
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Db 114 PLTNOEIPSSGSGFIMSEAGLITNAHVLTN-----QKIQVELSGARFATVKDID 167
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QY 105 KSDIATIKIHPKKLPVLLGHSADLRPGFVVAIGSPALONTTGTGIVTAOREGRE 164
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 168 HKLDLALIKIBEDTELPVLLGRSSDLRAGEFVVALGSPFSLQNTVTAIGIVTTORCGRE 227
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QY 165 LGLRSDMDYTQDAIINTGNSGGLVNDLDEVGINTLKVTAIGISFPAISDRITRFLTE 224
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 228 LGLRSDMDYTQDAIINTGNSGGLVNDLDEVGINTLKVTAIGISFPAISDRITRFLTE 287
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 225 FQDKQIK--DWKKRFIGIRKRTTPSLVDELKASNPDPPEVSSGIYQEVAPNSPSQGRG 281
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 288 YHERQLKGAFLQCKYGLGRMLPLTLNLQEWKQDDPEFPVSSGVFYEYQGSAAAS 347
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 282 GIQDDGIYKNGRPLVDSSELOEAVLTESPILLEVRGNDLLFSINPEV 333
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 348 GIRDHDIIVSINGQPVTTTVDVTEAVKNDPLSLIIVLGSQTLFLTPPEII 399
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-08-923-454A-6
; Sequence 6, Application US/08923454A
; Patent No. 6004794
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caretha
; APPLICANT: Lavi, George
; APPLICANT: Kattan, Eric
; APPLICANT: Clinkbeard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORIGINAL SOURCE: 24 Xaa = Arg or Cys
; ORIGINAL SOURCE: 278 Xaa = Ala or Val
US-08-923-454A-31
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RESULT 13
 US-08-923-454A-29
 Sequence 29, Application US/08923454A
 Patent No. 6004794
 GENERAL INFORMATION:
 APPLICANT: Creasy, Caretha
 APPLICANT: Livi, George
 APPLICANT: Karan, Eric
 APPLICANT: Clinkenbeard, Helen
 APPLICANT: Browne, Michael
 APPLICANT: Southan, Christopher
 TITLE OF INVENTION: HUMAN SERINE PROTEASE
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/923,454A

RESULT 14
 US-08-923-454A-4
 : Sequence 4, Application US/08923454A
 : Patent No. 6004794
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Creasy, Caretha
 : APPLICANT: Livi, George
 : APPLICANT: Kairan, Eric
 : APPLICANT: Clinkenbeard, Helen
 : APPLICANT: Browne, Michael
 : APPLICANT: Southan, Christopher
 :
 : TITLE OF INVENTION: HUMAN SERINE PROTEASE
 :
 : NUMBER OF SEQUENCES: 40
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESS: SmithKline Beecham Corporation
 : STREET: 709 Swedeland Road
 : CITY: King of Prussia
 : STATE: PA

```

? COUNTRY: USA
? ZIP: 19406
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/923,454A
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/025436
? FILING DATE: 06-SEPT-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Baumeister, Kirk
? REGISTRATION NUMBER: 33,833
? REFERENCE/DOCKET NUMBER: P50547
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610-270-5096
? TELEFAX: 610-270-5090
?
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 323 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
US-08-923-454A-4

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Query Match          33.6%; Score 564; DB 2; Length 323;
Best Local Similarity 59.9%; Pred. No. 3.9e-52;
Matches 109; Conservative 37; Mismatches 30; Indels 6; Gaps 1;

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DB 87 ASRSQYNFIADVVEKTAAPAVVYIELDRHPFLGREVPISNGSGFVVAADGLITNAHV 146
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QY 75 SSNSAAPGRQOLKVLQNGDSYEATIKDIDKSDIATIKHPKKLPVLLIGHSADLRPG 134
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 147 AD-----RRRVRLISGDTYEAVTAVDPVADITLRIQKEPPTLPGRSADVROG 200
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 135 EFVVAIGSPFALQNTTIGIVSTAQREGRELGLRDSMDYIQTDAIINYNGSGPLVND 194
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 201 EFVVAIGSPFALQNTTIGIVSSAQRPARDLGLPQTNVEYIQTDAIDFGNSGGLVNLV 260
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QY 195 GE 196
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DB 261 SE 262

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RESULT 15
US-08-923-454A-27
Sequence 27, Application US/08923454A
Patent No. 6004794

GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karren, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESSES:
ADDRESSES: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia

```

? STATE: PA
? COUNTRY: USA
? ZIP: 19406
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/923,454A
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/025436
? FILING DATE: 06-SEPT-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Baumeister, Kirk
? REGISTRATION NUMBER: 33,833
? REFERENCE/DOCKET NUMBER: P50547
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 610-270-5096
? TELEFAX: 610-270-5090
?
? INFORMATION FOR SEQ ID NO: 27:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 377 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: N-terminal
? ORIGINAL SOURCE:
US-08-923-454A-27

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Query Match          33.6%; Score 564; DB 2; Length 377;
Best Local Similarity 59.9%; Pred. No. 5e-52;
Matches 109; Conservative 37; Mismatches 30; Indels 6; Gaps 1;

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QY 15 SSRRYKFNFIADVVEKIAPAVVHIELFLRHPLEGRNVPLSSGGGFIMSEAGLIITNAHV 74
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DB 141 ASRSQYNFIADVVEKTAAPAVVYIELDRHPFLGREVPISNGSGFVVAADGLITNAHV 200
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 75 SSNSAAPGRQOLKVLQNGDSYEATIKDIDKSDIATIKHPKKLPVLLIGHSADLRPG 134
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 201 AD-----RRRVRLISGDTYEAVTAVDPVADITLRIQKEPPTLPGRSADVROG 254
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QY 135 EFVVAIGSPFALQNTTIGIVSTAQREGRELGLRDSMDYIQTDAIINYNGSGPLVND 194
   ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 255 EFVVAIGSPFALQNTTIGIVSSAQRPARDLGLPQTNVEYIQTDAIDFGNSGGLVNLV 314
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QY 195 GE 196
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DB 315 SE 316

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Search completed: February 21, 2006, 21:03:03
Job time : 48 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2006, 21:13:11 : Search time 163 Seconds
(without alignments)
856.166 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679
Sequence: 1 MHIALPASAGLHQLSSPRKY.....LEVVRGNDLLFSTAPEVVM 334

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1679	100.0	334	US-10-189-099A-2	Sequence 2, Appl1
2	1679	100.0	334	US-10-617-443B-2	Sequence 2, Appl1
3	1635	97.4	348	US-09-796-753-34	Sequence 34, Appl1
4	1635	97.4	453	US-09-796-753-32	Sequence 32, Appl1
5	1635	97.4	453	US-10-275-505-14	Sequence 14, Appl1
6	1635	97.4	453	US-10-381-820A-8	Sequence 8, Appl1
7	1635	97.4	453	US-10-485-313A-33	Sequence 33, Appl1
8	1635	97.4	453	US-11-140-224-14	Sequence 14, Appl1
9	1536	91.5	459	US-10-485-313A-27	Sequence 27, Appl1
10	1378	82.1	286	US-09-764-898-256	Sequence 256, App
11	1353.5	80.6	452	US-10-301-822-75	Sequence 79, Appl1
12	1117	66.5	357	US-09-485-313A-34	Sequence 34, Appl1
13	1105	65.8	330	US-09-764-898-184	Sequence 184, App
14	1057	63.0	363	US-10-485-313A-39	Sequence 39, Appl1
15	1034.5	61.6	447	US-10-104-047-2765	Sequence 2765, App
16	1034.5	61.6	480	US-10-170-385-355	Sequence 355, App
17	1034.5	61.6	480	US-10-772-636-48	Sequence 48, Appl1
18	1027.5	61.2	517	US-10-264-049-2310	Sequence 2310, App
19	994.5	59.2	405	US-09-925-298-552	Sequence 552, App
20	994.5	59.2	405	US-10-102-806-552	Sequence 552, App
21	890	53.0	476	US-09-935-390A-37	Sequence 37, Appl1
22	890	53.0	476	US-10-789-241-50	Sequence 50, Appl1
23	890	53.0	476	US-10-772-636-8	Sequence 8, Appl1
24	882	52.5	321	US-10-730-476A-52	Sequence 52, Appl1
25	882	52.5	321	US-10-730-476A-52	Sequence 52, Appl1
26	882	52.5	325	US-10-730-476A-44	Sequence 44, Appl1
27	882	52.5	325	US-10-730-476A-44	Sequence 44, Appl1

28	882	52.5	458	3	US-09-968-415-11	Sequence 11, Appl1
29	882	52.5	458	4	US-10-197-634-1	Sequence 1, Appl1
30	882	52.5	458	4	US-10-180-719-11	Sequence 11, Appl1
31	882	52.5	458	4	US-10-352-684A-10	Sequence 10, Appl1
32	882	52.5	458	6	US-11-045-577-11	Sequence 11, Appl1
33	882	52.5	529	4	US-10-216-667-5	Sequence 45, Appl1
34	862	51.3	325	4	US-10-730-476A-45	Sequence 46, Appl1
35	862	51.3	325	4	US-10-730-476A-47	Sequence 47, Appl1
36	862	51.3	325	4	US-10-730-476A-53	Sequence 53, Appl1
37	862	51.3	325	5	US-10-730-476A-53	Sequence 43, Appl1
38	862	51.3	325	5	US-10-730-476A-46	Sequence 46, Appl1
39	862	51.3	325	5	US-10-730-476A-47	Sequence 47, Appl1
40	862	51.3	325	5	US-10-730-476A-46	Sequence 53, Appl1
41	862	51.3	325	5	US-10-730-476A-53	Sequence 18, Appl1
42	854	50.9	178	3	US-09-969-384-18	Sequence 54, Appl1
43	689	41.0	221	4	US-10-730-476A-54	Sequence 54, Appl1
44	689	41.0	221	5	US-10-730-476A-54	Sequence 54, Appl1
45	689	41.0	225	4	US-10-730-476A-48	Sequence 48, Appl1

ALIGNMENTS

RESULT 1
US-10-189-099A-2
; Sequence 2, Application US/10189099A
; Publication No. US20040005659A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Cailin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/189, 099A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-099A-2

Query Match	100.0%	Score 1679	DB 4	Length 334
Best Local Similarity	100.0%	Pred. No. 4.5e-144	Indels 0	Gaps 0
Matches 334	Conservative	Mismatches 0	Indels 0	Gaps 0
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1	MHIALPASAGLHQLSSPRKFNFDVVEKIAPAVHIEFLRHPVPLSSGSGFI	60		
Q	61	MSEAGLITTNHVVSSNSAPRGQQLKVQLQNGDSYEATIKDIDKSDIATIKHPKKKL	120	
61	MSEAGLITTNHVVSSNSAPRGQQLKVQLQNGDSYEATIKDIDKSDIATIKHPKKKL	120		
Q	121	PVLLGHADLRPGFVVAIGSPFALQNTVTGISTNQRGRREGLDSDMDVYQOTAI	180	
121	PVLLGHADLRPGFVVAIGSPFALQNTVTGISTNQRGRREGLDSDMDVYQOTAI	180		
Q	181	INVGSGPLVNLDEVGINTLKTAGISPAISDRITRFLTEPQDKQIKDKKRFTIGI	240	
181	INVGSGPLVNLDEVGINTLKTAGISPAISDRITRFLTEPQDKQIKDKKRFTIGI	240		
Q	241	RNRITTPSLVDLKLKSNDDPEVSSGIYQGVAPNSPQKGGIQDGDIIIVKXNGPPLVDS	300	
241	RNRITTPSLVDLKLKSNDDPEVSSGIYQGVAPNSPQKGGIQDGDIIIVKXNGPPLVDS	300		
Q	301	SELQAVLTSPPLLEVRGNDLLFSTAPEVVM	334	
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RESULT 2
 US-10-617-443B-2
 ; Sequence 2, Application US/10617443B
 ; Publication No. US20050019777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Darrow, Andrew L
 ; APPLICANT: Q1, Jian-shen
 ; APPLICANT: Chen, Cailin
 ; APPLICANT: Andrade-Gordon, Patricia
 ; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
 ; FILE REFERENCE: ORT-1644
 ; CURRENT APPLICATION NUMBER: US/10/617,443B
 ; CURRENT FILING DATE: 2003-07-02
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 334
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-617-443B-2

Query Match 100.0%; Score 1679; DB 5; Length 334;
 Best Local Similarity 100.0%; Pred. No. 4, 5e-144;
 Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 MHIALPASAGLHQLSSPRYKFNFIADVVEKIAPAVVIHLEFLRHPFGFGRVPLSSGSGFT 60
 QY 61 MSEAGLIITNAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKL 120
 DB 61 MSEAGLIITNAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKL 120
 QY 121 PVLLGHSADLRGEFVVAIGSPFALONTTGTIVSTAOREGELGRSDMDYIOTDAI 180
 DB 121 PVLLGHSADLRGEFVVAIGSPFALONTTGTIVSTAOREGELGRSDMDYIOTDAI 180
 QY 181 INYNSGGPLVNDGEVIGINTLKTAGISFALPSDRITRFLTEFODKOIKMKKRFIGI 240
 DB 181 INYNSGGPLVNDGEVIGINTLKTAGISFALPSDRITRFLTEFODKOIKMKKRFIGI 240
 QY 241 RMRITPSLVDELKASNPDPPEVSSGIYQEVAPNSPSORGGIQQDDIIIVKNGRPLVDS 300
 DB 241 RMRITPSLVDELKASNPDPPEVSSGIYQEVAPNSPSORGGIQQDDIIIVKNGRPLVDS 300
 QY 301 SELOEAVLTESPILLEVRGNDLPSIAPEVVM 334
 DB 301 SELOEAVLTESPILLEVRGNDLPSIAPEVVM 334

RESULT 3
 US-09-796-753-34
 ; Sequence 34, Application US/09796753
 ; Publication No. US20030027998A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McCarthy, Sean A.
 ; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 7853-227-999
 ; CURRENT APPLICATION NUMBER: US/09/796,753
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 09/183,175
 ; PRIOR FILING DATE: 1998-10-30
 ; PRIOR APPLICATION NUMBER: 09/223,094
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/223,546
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/224,246
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/259,388
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/122,458
 ; PRIOR FILING DATE: 1999-03-01
 ; PRIOR APPLICATION NUMBER: 09/312,359

; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 09/336,536
 ; PRIOR FILING DATE: 1999-06-18
 ; PRIOR APPLICATION NUMBER: 09/342,687
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 09/345,464
 ; PRIOR FILING DATE: 1999-06-30
 ; PRIOR APPLICATION NUMBER: 09/365,164
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 09/399,723
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 09/409,634
 ; PRIOR FILING DATE: 1999-09-30
 ; PRIOR APPLICATION NUMBER: 09/471,179
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: 09/474,071
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/474,072
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/514,010
 ; PRIOR FILING DATE: 2000-02-25
 ; PRIOR APPLICATION NUMBER: 09/516,745
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 09/572,002
 ; PRIOR FILING DATE: 2000-05-14
 ; PRIOR APPLICATION NUMBER: 09/597,993
 ; PRIOR FILING DATE: 2000-06-19
 ; PRIOR APPLICATION NUMBER: 09/599,596
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 09/630,334
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: 09/606,565
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: 09/606,317
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: 09/665,666
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: 09/677,751
 ; PRIOR FILING DATE: 2000-09-30
 ; NUMBER OF SEQ ID NOS: 162
 ; SEQ ID NO 34
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Mouse
 US-09-796-753-34

Query Match 97.4%; Score 1635; DB 3; Length 348;
 Best Local Similarity 100.0%; Pred. No. 4, 8e-140;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GLHQLSSPRYKFNFIADVVEKIAPAVVIHLEFLRHPFGFGRVPLSSGSGFTMSEAGLIIT 69
 DB 24 GLHQLSSPRYKFNFIADVVEKIAPAVVIHLEFLRHPFGFGRVPLSSGSGFTMSEAGLIIT 69
 QY 70 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKL 129
 DB 84 NAHVSSNSAAPGRQOLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKL 129
 QY 130 DLRRGEFVVAIGSPFALONTTGTIVSTAOREGELGRSDMDYIOTDAI 203
 DB 144 DLRRGEFVVAIGSPFALONTTGTIVSTAOREGELGRSDMDYIOTDAI 203
 QY 190 LVNLDGEVIGINTLKTAGISFALPSDRITRFLTEFODKOIKMKKRFIGIRMTTIPSL 249
 DB 204 LVNLDGEVIGINTLKTAGISFALPSDRITRFLTEFODKOIKMKKRFIGIRMTTIPSL 263
 QY 250 VDELKASNPDPPEVSSGIYQEVAPNSPSORGGIQQDDIIIVKNGRPLVDSSELOEAVLT 309
 DB 264 VDELKASNPDPPEVSSGIYQEVAPNSPSORGGIQQDDIIIVKNGRPLVDSSELOEAVLT 323
 QY 310 ESPILLEVRGNDLPSIAPEVVM 334
 DB 324 ESPILLEVRGNDLPSIAPEVVM 348

RESULT 4

US-09-796-753-32

; Sequence 32, Application US/09796753

; Publication No. US20030027998A1

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A.

; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

; FILE REFERENCE: 7853-227-999

; CURRENT APPLICATION NUMBER: US/09/796,753

; CURRENT FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 09/183,175

; PRIOR FILING DATE: 1998-10-30

; PRIOR APPLICATION NUMBER: 09/223,094

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/223,546

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/224,246

; PRIOR FILING DATE: 1998-12-30

; PRIOR APPLICATION NUMBER: 09/259,388

; PRIOR FILING DATE: 1999-02-26

; PRIOR APPLICATION NUMBER: 60/122,458

; PRIOR FILING DATE: 1999-03-01

; PRIOR APPLICATION NUMBER: 09/312,359

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 09/336,536

; PRIOR FILING DATE: 1999-06-18

; PRIOR APPLICATION NUMBER: 09/342,687

; PRIOR FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: 09/345,464

; PRIOR FILING DATE: 1999-06-30

; PRIOR APPLICATION NUMBER: 09/365,164

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: 09/399,723

; PRIOR FILING DATE: 1999-09-20

; PRIOR APPLICATION NUMBER: 09/409,634

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: 09/471,179

; PRIOR FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 09/474,071

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: 09/474,072

; PRIOR FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: 09/514,010

; PRIOR FILING DATE: 2000-02-25

; PRIOR APPLICATION NUMBER: 09/516,745

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 09/572,002

; PRIOR FILING DATE: 2000-05-14

; PRIOR APPLICATION NUMBER: 09/597,993

; PRIOR FILING DATE: 2000-06-19

; PRIOR APPLICATION NUMBER: 09/599,596

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 09/630,334

; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: 09/606,565

; PRIOR FILING DATE: 2000-06-29

; PRIOR APPLICATION NUMBER: 09/606,317

; PRIOR FILING DATE: 2000-06-29

; PRIOR APPLICATION NUMBER: 09/665,666

; PRIOR FILING DATE: 2000-09-20

; PRIOR APPLICATION NUMBER: 09/677,751

; PRIOR FILING DATE: 2000-09-30

; NUMBER OF SEQ ID NOS: 162

; SEQ ID NO 32

; LENGTH: 453

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-796-753-32

Query Match 97.4%; Score 1635; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.1e-140;

Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 10 GHHQSSRRYKFNFLADYVEKIAPAVYHIEFLRHPLEGRVVPVSSGGGFTMSEAGLIT 69
DB 129 GHQSSRRYKFNFLADYVEKIAPAVYHIEFLRHPLEGRVVPVSSGGGFTMSEAGLIT 188
QY 70 NAHVSSNSAAPGRQQLKVQKQNGSDSYEATIKDKSDITIKHPKKLPVLLGHSA 129
DB 189 NAHVSSNSAAPGRQQLKVQKQNGSDSYEATIKDKSDITIKHPKKLPVLLGHSA 248
QY 130 DLRPGEFVVAIGSPFALQNTVTGIVSTAQEGREGLRSDSDMDVYIQTDALINYGNSGP 189
DB 249 DLRPGEFVVAIGSPFALQNTVTGIVSTAQEGREGLRSDSDMDVYIQTDALINYGNSGP 308
QY 190 LVNLDGEVIGINTLKTATGIFALPSDITFLTFEPQKQIKDWKREIGIRMTITPSL 249
DB 309 LVNLDGEVIGINTLKTATGIFALPSDITFLTFEPQKQIKDWKREIGIRMTITPSL 368
QY 250 VDELKASNPDPPEVSSGIYQVQVAPNSPQSGIQQDGIYKNGRPLVDSSELOEAVLT 309
DB 369 VDELKASNPDPPEVSSGIYQVQVAPNSPQSGIQQDGIYKNGRPLVDSSELOEAVLT 428
QY 310 ESPLLLEVRGNDLLFSLAPEVVM 334
DB 429 ESPLLLEVRGNDLLFSLAPEVVM 453
```

RESULT 5

US-10-275-505-14

; Sequence 14, Application US/10275505

; Publication No. US20040081961A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: DELEGANE, Angelo M.; LAL, Preeti G.

; APPLICANT: HAFALIA, April J.A.; PATTERSON, Chandra

; APPLICANT: WALIA, Nardinder K.; KEARNEY, Liam

; APPLICANT: TRIBOULEY, Catherine M.; KHAN, Farrah A.

; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.

; APPLICANT: AZIMZAI, Yalda; ELIOTY, Vicki S.

; APPLICANT: NGUYEN, Danielle B.; GANDHI, Ameeta R.

; APPLICANT: YANG, Junming; HERNANDEZ, Roberto

; APPLICANT: POLICKY, Jennifer L.; LU, Dyung Aina M.

; APPLICANT: REDDY, Roopa M.; YUE, Henry

; APPLICANT: TANG, Y. Tom

; TITLE OF INVENTION: PROTEASES

; FILE REFERENCE: PI-0085 USN

; CURRENT APPLICATION NUMBER: US/10/275,505

; CURRENT FILING DATE: 2002-11-04

; PRIOR APPLICATION NUMBER: PCT/US01/14651

; PRIOR FILING DATE: 2001-05-04

; PRIOR APPLICATION NUMBER: 60/209,402

; PRIOR FILING DATE: 2000-06-01

; PRIOR APPLICATION NUMBER: 60/207,477

; PRIOR FILING DATE: 2000-05-25

; PRIOR APPLICATION NUMBER: 60/205,803

; PRIOR FILING DATE: 2000-05-17

; PRIOR APPLICATION NUMBER: 60/203,566

; PRIOR FILING DATE: 2000-05-11

; PRIOR APPLICATION NUMBER: 60/202,082

; PRIOR FILING DATE: 2000-05-04

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PERL Program

; SEQ ID NO 14

; LENGTH: 453

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; OTHER INFORMATION: Incyte ID No: 7474343CD1

; US-10-275-505-14

Query Match 97.4%; Score 1635; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.1e-140;

	Matches	325; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
Qy	10	GLHQLSSRYRYKFNFIADVYVEKIAAPAVVHI	ELFLRHPLFGRNVP	PLSSGSGGFIMSEAGLIIT	69	
Db	129	GLHQLSSRYRYKFNFIADVYVEKIAAPAVVHI	ELFLRHPLFGRNVP	PLSSGSGGFIMSEAGLIIT	188	
Qy	70	NAHVYSSNSAAPGRQQLKVQLONGSYEATTKD	IDDKSDIATIKTHPKKKL	PVLLLGSA	129	
Db	189	NAHVYSSNSAAPGRQQLKVQLONGSYEATTKD	IDDKSDIATIKTHPKKKL	PVLLLGSA	248	
Qy	130	DLRGEFVVAIGSPPALQNTVTTGIVSTAOREG	RELGLRDSMDYITQDIAI	INYNSSGP	189	
Db	249	DLRGEFVVAIGSPPALQNTVTTGIVSTAOREG	RELGLRDSMDYITQDIAI	INYNSSGP	308	
Qy	190	LVNIDGEVIGINTLKVTAIGISPAIPSDRI	ITRFLTEFQDKQIKDWKKRP	IGIRMRITPSL	249	
Db	309	LVNIDGEVIGINTLKVTAIGISPAIPSDRI	ITRFLTEFQDKQIKDWKKRP	IGIRMRITPSL	368	
Qy	250	VDELKASNPDPPEVSSGIVYQEVAPNS	SSQSGIIDDGII	IYKAKRPLVDSSELOEAVLT	309	
Db	369	VDELKASNPDPPEVSSGIVYQEVAPNS	SSQSGIIDDGII	IYKAKRPLVDSSELOEAVLT	428	
Qy	310	ESPLLEVRGRNDLLFSIAPEVVM	334			
Db	429	ESPLLEVRGRNDLLFSIAPEVVM	453			

```

RESULT 6
US-10-381-820A-8
: Sequence 8, Application US/10381820A
: Publication No. US20040142333A1
GENERAL INFORMATION:
APPLICANT: Destun, Lu
APPLICANT: Song, Ho Yeong
APPLICANT: Su, Eric Wen
APPLICANT: Wang, He
FILE OF INVENTION: Novel Secreted Proteins and Their Uses
FILE REFERENCE: X-13974
CURRENT APPLICATION NUMBER: US/10/381,820A
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 8
LENGTH: 453
TYPE: PRT
ORGANISM: Homo sapiens
US-10-381-820A-8

```

Query Match	97.4%;	Score 1635;	DB 4;	Length 453;
Best Local Similarity	100.0%;	Pred. NO. 7.1e-140;		
Matches 325;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	10	GLHQLSSPRKYENFIADVEKIAIAPVAHIIEFLRHPLFGRNVPPLSSGGFIMSEAGLIIT	69	
Db	129	GLHQLSSPRKYENFIADVEKIAIAPVAHIIEFLRHPLFGRNVPPLSSGGFIMSEAGLIIT	188	
QY	70	NAHVSSNSAAPGRHQLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA	129	
Db	189	NAHVSSNSAAPGRHQLKVQLQNGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA	248	
QY	130	DLRGEREVAIAGSPFALQNTYTTGTIVTAQNEGBELGLRDSMDMYIQTDALINNGSGP	189	
Db	249	DLRGEREVAIAGSPFALQNTYTTGTIVTAQNEGBELGLRDSMDMYIQTDALINNGSGP	308	
QY	190	LVNLDDGEVIGINTLKTAGISFALPSDRITFLREFODKQIKDKKKRPIGIRMKTTIPSL	249	
Db	309	LVNLDDGEVIGINTLKTAGISFALPSDRITFLREFODKQIKDKKKRPIGIRMKTTIPSL	368	
QY	250	VDELKASNPDPFEVSSGIVQOEVAIAPNSBQRCGCIQDGDIIYKVAAGRPLVDSSEIQEAVLT	309	
Db	369	VDELKASNPDPFEVSSGIVQOEVAIAPNSBQRCGCIQDGDIIYKVAAGRPLVDSSEIQEAVLT	428	
QY	310	ESPLLLEVRGNDLLFSAIEVVM	334	

Db 429 ESPLLEVRGNDLFSIAPEVM 453

```

RESULT 7
US-10-485-313A-33
: Sequence 33, Application US/10465313A
: Publication No. US20050059002A1
: GENERAL INFORMATION:
: APPLICANT: NIE, Guiying
: APPLICANT: SALAMONSEN, Loie Adrienne
: APPLICANT: Li, Yang
: APPLICANT: HAMPTON, Anne Lorraine
: APPLICANT: FINDLAY, John Kerr
: TITLE OF INVENTION: Novel Serine Protease
: FILE REFERENCE: 31633-200357
: CURRENT APPLICATION NUMBER: US/10/485,313A
: CURRENT FILING DATE: 2004-01-30
: PRIOR APPLICATION NUMBER: PCT/AU02/01010
: PRIOR FILING DATE: 2002-07-30
: PRIOR APPLICATION NUMBER: P676707
: PRIOR FILING DATE: 2001-07-30
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 33
: LENGTH: 453
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-485-313A-33

```

Query Match	97.4%	Score 1635;	DB 5;	Length 453;
Best Local Similarity	100.0%	Pred. No. 7.1e-140;		
Matches 325;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GLHOLSSPRYKKNFADVVEKIAAPVAHIELFLHPLFGNNVPLSSSSGGTMSDEAGLIT	69
Db	129	GLHOLSSPRYKKNFADVVEKIAAPVAHIELFLHPLFGNNVPLSSSSGGTMSDEAGLIT	188
Qy	70	NAHVVSNSNAAPGRQOLKVOLQNGDSYEATIKDIDKSDIATIKIHPKKKLPLYLLGHSA	129
Db	189	NAHVVSNSNAAPGRQOLKVOLQNGDSYEATIKDIDKSDIATIKIHPKKKLPLYLLGHSA	248
Qy	130	DLRPEEPVAAAGSPALQNTVTTGTIVSTPAQEGESELGRDSMDVYIOTDAIIVNGSGGP	189
Db	249	DLRPEEPVAAAGSPALQNTVTTGTIVSTPAQEGESELGRDSMDVYIOTDAIIVNGSGGP	308
Qy	190	LVNLDEVIAGINTLKVTAIGISPAIPSDRITRELFTEPODKOIKOMKKRFIGIRMRITTPSL	249
Db	309	LVNLDEVIAGINTLKVTAIGISPAIPSDRITRELFTEPODKOIKOMKKRFIGIRMRITTPSL	368
Qy	250	VDELKASNPDPPEVSSGIYVOEVAPNPSPOGGIODDIDIVKVNGRPLVDSSELOEAVLT	309
Db	369	VDELKASNPDPPEVSSGIYVOEVAPNPSPOGGIODDIDIVKVNGRPLVDSSELOEAVLT	428
Qy	310	ESPILLLEVRKNDLLFSIAPEVVM	334
Db	429	ESPILLLEVRKNDLLFSIAPEVVM	453

US-11-140-224-14
 ; Sequence 14, Application US/111440224
 ; Publication No. US20050227280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: DELBEGANNE, Angelo M.; IAL, Preeti G.
 ; APPLICANT: HAPFALL, April J.A.; PATTERSON, Chandra
 ; APPLICANT: WALIA, Nandinder K.; KEARNEY, Liam
 ; APPLICANT: TRIPOURIEY, Catherine M.; KHAN, Farrah A.
 ; APPLICANT: YAO, Monique G.; BAUGHN, Mariah R.
 ; APPLICANT: AZIMZAI, Jalid; ELLIOTT, Vicki S.
 ; APPLICANT: NGUYEN, Daniel B.; GANDHI, Ameena R.
 ; APPLICANT: YANG, Junning; HERNANDEZ, Roberto

```
APPLICANT: POLICKY, Jennifer L.; LU, Dyrung Aina M.
APPLICANT: REDDY, Roopa M.; YUE, Henry
APPLICANT: TANG, Y. Tom
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PI-0085 USN
CURRENT APPLICATION NUMBER: US/11/140,224
CURRENT FILING DATE: 2005-05-31
PRIORITY APPLICATION NUMBER: US/10/275,505
PRIORITY FILING DATE: 2002-11-04
PRIORITY APPLICATION NUMBER: PCT/US01/14651
PRIORITY FILING DATE: 2001-05-04
PRIORITY APPLICATION NUMBER: 60/209,402
PRIORITY FILING DATE: 2000-06-01
PRIORITY APPLICATION NUMBER: 60/207,477
PRIORITY FILING DATE: 2000-05-25
PRIORITY APPLICATION NUMBER: 60/205,803
PRIORITY FILING DATE: 2000-05-17
PRIORITY APPLICATION NUMBER: 60/203,566
PRIORITY FILING DATE: 2000-05-11
PRIORITY APPLICATION NUMBER: 60/202,082
PRIORITY FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 453
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7474343CD1
US-11-140-224-14
```

```
Query Match 97.4%; Score 1635; DB 6; Length 453;
Best Local Similarity 100.0%; Pred. No. 7.1e-140;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 10 GLHQLSSPRKPFNFADVVEKIPAVVHIELFRLHPLFGHNVPLSSGSGFIMSEAGLIIT 69
Db 129 GLHQLSSPRKPFNFADVVEKIPAVVHIELFRLHPLFGHNVPLSSGSGFIMSEAGLIIT 188
Qy 70 NAHVSSNSAAPGRQQLKVQLQNGDSYEATIKDIDKSDIATIKIHKKKL PVLILGHS 129
Db 189 NAHVSSNSAAPGRQQLKVQLQNGDSYEATIKDIDKSDIATIKIHKKKL PVLILGHS 248
Qy 130 DLRFGEFVAVAGSPALQNTVTGIVSTAQREGRELGRSDMDYIQTDAIINYNGSGP 189
Db 249 DLRFGEFVAVAGSPALQNTVTGIVSTAQREGRELGRSDMDYIQTDAIINYNGSGP 308
Qy 190 LVNLGDEVIGINTLKVTAIGISPAISDRITRFLTEFODKQIKDKKRFIIGIRMTITPSL 249
Db 309 LVNLGDEVIGINTLKVTAIGISPAISDRITRFLTEFODKQIKDKKRFIIGIRMTITPSL 368
Qy 250 VDELKASNPDPPEVSSGIYQEVAPNSPSQGGIQQGDIIVKNGRPVLDSSSELQEAVALT 309
Db 369 VDELKASNPDPPEVSSGIYQEVAPNSPSQGGIQQGDIIVKNGRPVLDSSSELQEAVALT 428
Qy 310 ESPLLLEVRGNDLLFSIAPREVVM 334
Db 429 ESPLLLEVRGNDLLFSIAPREVVM 453
```

```
RESULT 9
US-10-485-313a-27
Sequence 27, Application US/10485313a
GENERAL INFORMATION:
APPLICANT: NIE, Guiying
APPLICANT: SALAMONSEN, Lois Adrienne
APPLICANT: LI, Ying
APPLICANT: HAMPTON, Anne Lorraine
APPLICANT: FINDLAY, John Kerr
TITLE OF INVENTION: Novel Serine Protease
FILE REFERENCE: 31633-200357
```

```
CURRENT APPLICATION NUMBER: US/10/485,313A
CURRENT FILING DATE: 2004-01-30
PRIORITY APPLICATION NUMBER: PCT/AU02/01010
PRIORITY FILING DATE: 2002-07-30
PRIORITY APPLICATION NUMBER: PR6707
PRIORITY FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 459
TYPE: PRT
ORGANISM: Mus musculus
US-10-485-313a-27
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Query Match 91.5%; Score 1536; DB 5; Length 459;
Best Local Similarity 92.6%; Pred. No. 7.4e-131;
Matches 302; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
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```
Qy 9 AGLHQLSSPRKPFNFADVVEKIPAVVHIELFRLHPLFGHNVPLSSGSGFIMSEAGLIIT 68
Db 134 AGLHQLSSPRKPFNFADVVEKIPAVVHIELFRLHPLFGHNVPLSSGSGFIMSEAGLIIT 193
Qy 69 TNAHVSSNSAAPGRQQLKVQLQNGDSYEATIKDIDKSDIATIKIHKKKL PVLILGHS 128
Db 194 TNAHVSSNSAAPGRQQLKVQLQNGDSYEATIKDIDKSDIATIKIHKKKL PVLILGHS 253
Qy 129 ADLRFGEFVAVAGSPALQNTVTGIVSTAQREGRELGRSDMDYIQTDAIINYNGSGP 188
Db 254 ADLRFGEFVAVAGSPALQNTVTGIVSTAQREGRELGRSDMDYIQTDAIINYNGSGP 313
Qy 189 LVNLGDEVIGINTLKVTAIGISPAISDRITRFLTEFODKQIKDKKRFIIGIRMTITPS 248
Db 314 LVNLGDEVIGINTLKVTAIGISPAISDRITRFLTEFODKQIKDKKRFIIGIRMTITPS 373
Qy 249 LVDELKASNPDPPEVSSGIYQEVAPNSPSQGGIQQGDIIVKNGRPVLDSSSELQEAVAL 308
Db 374 LVDELKASNPDPPEVSSGIYQEVAPNSPSQGGIQQGDIIVKNGRPVLDSSSELQEAVAL 433
Qy 309 TESPLLEVRGNDLLFSIAPREVVM 334
Db 434 TESPLLEVRGNDLLFSIAPREVVM 459
```

```
RESULT 10
US-09-764-898-256
Sequence 256, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P0201
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 311
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 256
LENGTH: 286
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (32)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (35)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (42)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (104)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
```


US-09-764-898-256

Query Match 82.1%; Score 1378; DB 3; Length 286;
Best Local Similarity 98.6%; Pred. No. 9e-117;
Matches 275; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 56 GSGFMSEAGLITITNAHVSSNSAAPGQOLKVQONQDSYEATIKOIDKKSIDIATIKIH 115
DB 8 GSGFMSEAGLITITNAHVSSNSAAPGQOLKVQONQDSYEATIKOIDKKSIDIATIKIH 67
QY 116 PKKKLPVLLGHSADLRPEEFVAIGSPFALONTTGTIVSTAOEGREGLGRSDMDYI 175
DB 68 PKKKLPVLLGHSADLRPEEFVAIGSPFALONTTGTIVSTAOEGREGLGRSDMDYI 127
QY 176 QTDALINGSGGFLVNLDEVIQINTLKVTAIGISPAISDRITRFLTEFODKOIDKMK 235
DB 128 QTDALINGSGGFLVNLDEVIQINTLKVTAIGISPAISDRITRFLTEFODKOIDKMK 187
QY 236 RPTGIMRTTTPSLVDELKASNDPEVSGIYVQEVANSPSQRGCIODGDIIVKNGR 295
DB 188 RPTGIMRTTTPSLVDELKASNDPEVSGIYVQEVANSPSQRGCIODGDIIVKNGR 247
QY 296 PLVDSSELQEAVALTESPILLEVRGNDLLFSIAPEVVM 334
DB 248 PLVDSSELQEAVALTESPILLEVRGNDLLFSIAPEVVM 286

RESULT 11

US-10-301-822-79
Sequence 79, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MP001-029P2RUM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 452
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-79

Query Match 80.6%; Score 1353.5; DB 4; Length 452;
Best Local Similarity 86.1%; Pred. No. 3e-114;
Matches 285; Conservative 4; Mismatches 29; Indels 13; Gaps 3;

QY 10 GLHQLSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFGFNVPLSSGSGFIMSEAGLIIT 69
DB 129 GLHQLSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFGFNVPLSSGSGFIMSEAGLIIT 188
QY 70 NAHVSSNSAAPGQOLKVQONQDSYEATIKOIDKKSIDIATIKIHPPKKLPVLLGSHA 129
DB 189 NAHVSSNSAAPGQOLKVQONQDSYEATIKOIDKKSIDIATIKIHPPKKLPVLLGSHA 248
QY 130 DLRRGEFVAIGSPFALONTTGTIVST-----AQREGREGLGRSDMDYIQTDAIINY 183

DB 249 DLRRGSLMWPSESLRPTREHS-DNGIIVALPSGQAGAPPGIRHGHTRM-----PSSNY 301

QY 184 GNSGGFLVNLDEVIQINTLKVTAIGISPAISDRITRFLTEFODKOIDKKSIDIATIKIH 243

DB 302 GNSGGFLVNLDEVIQINTLKVTAIGISPAISDRITRFLTEFODKOIDKKSIDIATIKIH 361

QY 244 TTPSLVDELKASNDPEVSGIYVQEVANSPSQRGCIODGDIIVKNGRPLVDSSEL 303

DB 362 TTPSLVDELKASNDPEVSGIYVQEVANSPSQRGCIODGDIIVKNGRPLVDSSEL 421

QY 304 QEAVALTESPILLEVRGNDLLFSIAPEVVM 334

DB 422 QEAVALTESPILLEVRGNDLLFSIAPEVVM 452

RESULT 12

US-10-485-313A-34
Sequence 34, Application US/10485313A
Publication No. US20050059002A1
GENERAL INFORMATION:
APPLICANT: NIE, Guiying
APPLICANT: SALAMONSEN, Lois Adrienne
APPLICANT: LI, Ying
APPLICANT: HAMPTON, Anne Lorraine
APPLICANT: FINDLAY, John Kerr
TITLE OF INVENTION: NOVEL Serine Protease
FILE REFERENCE: 31633-200357
CURRENT APPLICATION NUMBER: US/10/485,313A
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: PCT/NO02/01010
PRIOR FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: PR6707
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 34
LENGTH: 357
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-313A-34

Query Match 66.5%; Score 1117; DB 5; Length 357;
Best Local Similarity 100.0%; Pred. No. 7.1e-93;
Matches 222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GLHQLSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFGFNVPLSSGSGFIMSEAGLIIT 69

DB 129 GLHQLSSPRYKFNFIADVVEKIAPAVYHIELFLRHPFGFNVPLSSGSGFIMSEAGLIIT 188

QY 70 NAHVSSNSAAPGQOLKVQONQDSYEATIKOIDKKSIDIATIKIHPPKKLPVLLGSHA 129

DB 189 NAHVSSNSAAPGQOLKVQONQDSYEATIKOIDKKSIDIATIKIHPPKKLPVLLGSHA 248

QY 130 DLRRGEFVAIGSPFALONTTGTIVSTAOEGREGLGRSDMDYIQTDAIINYNSGAP 189

DB 249 DLRRGEFVAIGSPFALONTTGTIVSTAOEGREGLGRSDMDYIQTDAIINYNSGAP 308

QY 190 LVNLDEVIQINTLKVTAIGISPAISDRITRFLTEFODKOIDK 221

DB 309 LVNLDEVIQINTLKVTAIGISPAISDRITRFLTEFODKOIDK 350

RESULT 13

US-09-764-898-184
Sequence 184, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P201
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17

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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 184
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (244)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (265)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-184

Query Match          65.8%; Score 1105; DB 3; Length 330;
Best Local Similarity 99.1%; Pred. No. 7.9e-92;
Matches 220; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GLHQLSSPRYKFNFIADYVEKIAPAVVAHIELFLRHPPLGRNVPLSSGSGFTMSEGLIIT 69
Db 102 GLHQLSSPRYKFNFIADYVEKIAPAVVAHIELFLRHPPLGRNVPLSSGSGFTMSEGLIIT 161
Qy 70 NAHVSSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 129
Db 162 NAHVSSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 221
Qy 130 DLRRGEFVVAIGSPFALONTVTTGIVSTAOREGRELGRSDMDYIOTDAIINYNSGSP 189
Db 222 DLRRGEFVVAIGSPFALONTVTTGIVSTAOREGRELGRSDMDYIOTDAIINYNSGSP 281
Qy 190 LVNLDEVIQINTLKVTAIGISFALPSDRITRFLTEFODKOIK 231
Db 282 LVNLDEVIQINTLKVTAIGISFALPSDRITRFLTEFODKOIK 323

RESULT 14
US-10-485-313A-39
; Sequence 39, Application US/10485313A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guiling
; APPLICANT: SALAMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 39
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-485-313A-39

Query Match          63.0%; Score 1057; DB 5; Length 363;
Best Local Similarity 92.8%; Pred. No. 2.1e-87;
Matches 207; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 9 AGHQLSSPRYKFNFIADYVEKIAPAVVAHIELFLRHPPLGRNVPLSSGSGFTMSEGLIIT 68
Db 134 SGLHQLTSPRYKFNFIADYVEKIAPAVVAHIELFLRHPPLGRNVPLSSGSGFTMSEGLIIV 193
Qy 69 TNAHVSSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 128
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Db 194 TNAHVSSNSAAPGRQQLKVQLONGDAYEATIKDIDKSDIATIVIHPPKKLPVLLGHSA 253
Qy 129 ADLRGEFVVAIGSPFALONTVTTGIVSTAOREGRELGRSDMDYIOTDAIINYNSGSP 188
Db 254 ADLRGEFVVAIGSPFALONTVTTGIVSTAOREGRELGRSDMDYIOTDAIINYNSGSP 313
Qy 189 LVNLDEVIQINTLKVTAIGISFALPSDRITRFLTEFODKOIK 231
Db 314 LVNLDEVIQINTLKVTAAGISFALPSDRITRFLTEFONKIVK 356

RESULT 15
US-10-104-047-2765
; Sequence 2765, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2765
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-2765

Query Match          61.6%; Score 1034.5; DB 4; Length 447;
Best Local Similarity 62.1%; Pred. No. 3.2e-85;
Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

Qy 10 GLHQLSSPRYKFNFIADYVEKIAPAVVAHIELFLRHPPLGRNVPLSSGSGFTMSEGLIIT 69
Db 125 GQBDPNSLRHKCNFIADYVEKIAPAVVAHIELFLRHPPLGRNVPLSSGSGFTMSEGLIIV 184
Qy 70 NAHVSSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 129
Db 185 NAHVSSNSAAPGRQQLKVQLONGDSYEATIKDIDKSDIATIKIHPKKKLPVLLGHSA 238
Qy 130 DLRRGEFVVAIGSPFALONTVTTGIVSTAOREGRELGRSDMDYIOTDAIINYNSGSP 189
Db 239 ELRRGEFVVAIGSPFALONTVTTGIVSTAOREGRELGRSDMDYIOTDAIINYNSGSP 298
Qy 190 LVNLDEVIQINTLKVTAIGISFALPSDRITRFLTEFODKOIKD--WKREFGIRMRIT 246
Db 299 LVNLDEVIQINTLKVTAIGISFALPSDKIKFLTSHDRQAKGAIYTKKXITGIRMSLT 358
Qy 247 PSYDELKASNPDEPEVSSGIYQEVAPNSPDRGIGDGIIVKNGRPLVDSSELQEA 306
Db 359 SSXAKELKDRDRDPDVISGAYIIEVYPTPAKAGLKENDVIIISINGQSVASANDVSDV 418
Qy 307 VLTESPLLETRGRNDLLFSIABEV 333
Db 419 IKRESTLMVVRKGNEDIMITVPEEI 445

Search completed: February 21, 2006, 21:16:20
Job time : 164 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 21, 2006, 21:13:46 ; Search time 18 Seconds

(without alignments)
264.225 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679
Sequence: 1 MHLLPAPASGHLQSSPRK.....LEVRGNDLLFSTAPVVM 334

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 108093 seqs, 14239677 residues

Total number of hits satisfying chosen parameters: 108093

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	1353.5	80.6	452	7	US-11-186-284-79
2	1034.5	61.6	447	7	US-11-072-512-2765
3	1034.5	61.6	480	6	US-10-821-234-1465
4	882	52.5	458	7	US-11-183-914-11
5	535	31.9	109	7	US-11-053-076-59
6	496	29.5	100	7	US-11-107-096-78
7	414	24.7	499	6	US-10-467-657-2096
8	410	24.4	474	6	US-11-098-686-10591
9	360.5	21.5	441	6	US-10-454-437-56
10	335.5	20.0	423	7	US-11-074-176-4
11	318	18.9	317	6	US-10-793-626-1824
12	260.5	15.5	493	6	US-10-793-626-1832
13	259.5	15.5	115	6	US-10-485-788A-774
14	259.5	15.5	115	7	US-11-053-076-152
15	239	12.2	101	7	US-11-107-096-77
16	214.5	12.8	99	7	US-11-107-096-79
17	204	12.2	100	7	US-11-107-096-1
18	200.5	11.9	97	7	US-11-053-076-60
19	189	11.3	109	6	US-10-485-788A-805
20	189	11.3	109	7	US-11-053-076-188
21	128	7.6	397	6	US-10-454-437-60
22	122	7.3	238	6	US-10-485-517-191
23	120	7.1	217	7	US-11-019-711-136
24	116.5	6.9	239	6	US-10-485-517-192
25	116.5	6.9	239	6	US-10-485-517-195

26	116.5	6.9	239	6	US-10-485-517-323	Sequence 323, App
27	115.5	6.9	241	6	US-10-485-517-189	Sequence 189, App
28	114	6.8	180	6	US-10-485-517-194	Sequence 194, App
29	114	6.8	180	6	US-10-485-517-322	Sequence 322, App
30	113.5	6.8	247	6	US-10-485-517-190	Sequence 190, App
31	111.5	6.6	227	7	US-11-151-601-36	Sequence 36, App
32	111.5	6.6	249	7	US-11-151-601-28	Sequence 28, App
33	111.5	6.6	251	7	US-11-151-601-27	Sequence 27, App
34	107	6.4	254	6	US-10-485-517-188	Sequence 188, App
35	107	6.4	1183	7	US-11-115-639-18	Sequence 18, App
36	106	6.3	1183	7	US-11-115-639-15	Sequence 15, App
37	106	6.3	1183	7	US-11-115-639-17	Sequence 17, App
38	105	6.3	2759	6	US-10-453-372-168	Sequence 168, App
39	104	6.2	1183	7	US-11-115-639-13	Sequence 13, App
40	103	6.1	648	6	US-10-793-626-568	Sequence 568, App
41	100	6.0	1183	7	US-11-115-639-16	Sequence 16, App
42	100	6.0	4384	6	US-10-821-234-1120	Sequence 1120, App
43	99.5	5.9	282	6	US-10-793-626-364	Sequence 364, App
44	98.5	5.9	1183	7	US-11-115-639-14	Sequence 14, App
45	97.5	5.8	442	7	US-11-098-686-11368	Sequence 11368, A

ALIGNMENTS

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RESULT 1
US-11-186-284-79
; Sequence 79, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPM01-02952RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; PRIOR FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-79

Query Match      80.6%   Score 1353.5; DB 7; Length 452;
Best Local Similarity 86.1%; Pred. No. 8.8e-108;
Matches 285; Conservative 4; Mismatches 23; Indels 13; Gaps 3;

QY      10  GLHQLSSPRYKFNFIADYVEKIPAVVHIEFLRRHPLFGRNVPLSSGSGFTMSEAGLIIT 69
DB      129  GLHQLSSPRYKFNFIADYVEKIPAVVHIEFLRRHPLFGRNVPLSSGSGFTMSEAGLIIT 188
QY      70  NHHVSSNSAARGROQLNVOQLNGDSYRATIKDKDKSDIATIKHPKKKIPVLLGGHSA 129
DB      189  NHHVSSNSAARGROQLNVOQLNGDSYRATIKDKDKSDIATIKHPKKKIPVLLGGHSA 248
QY      130  DLRPFEEVVAIGSPALQNTVTTGIVST-----AQRGREGIQLRDSMDYIQTDALINY 183
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Db 249 DLAVGSLMPSESLRPTREHS-DNGIYVALPSGGGQAGPGLRHGHTRRM-----PSNVY 301
QY 184 GNSGGPLVNLDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIKKKKFIIGIR 243
Db 302 GNSGGPLVNLDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIKKKKFIIGIR 361
QY 244 TTPSLVDELKASNPDPPEVSSGIYVOEVAPNSPSQSGIQQDGIYKNGRPLVDSSEL 303
Db 362 TTPSLVDELKASNPDPPEVSSGIYVOEVAPNSPSQSGIQQDGIYKNGRPLVDSSEL 421
QY 304 QEAULTESPILLEVRGNDLFLSIAPEVVM 334
Db 422 QEAULTESPILLEVRGNDLFLSIAPEVVM 452

RESULT 2
US-11-072-512-2765
; Sequence 2765, Application US/11072512
; Publication No. US2006002945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YUKI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOTIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOCYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072, 512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350, 978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2765
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2765

Query Match 61.6%; Score 1034.5; DB 7; Length 447;
Best Local Similarity 62.1%; Pred. No. 1.3e-80;
Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

QY 10 GLHQLSPRYKPNFADVVEKIAPAVVHIELFLRHPLEGRVNPVLSGSGFIMSEAGLIT 69
Db 125 GQEDPNSLRHKNFADVVEKIAPAVVHIELFLRHPLEGRVNPVLSGSGFIMSEAGLIT 184
QY 70 NAHVSSNSAAPGRQOLKVQLONGSDYEATIKDIDKSDIATIKIHPKKKLPLVLLGHSA 129
Db 185 NAHVVTN-----KRVVVELKNGATYEAKIKDVDEKADIALIKIDHGGKLVLLGRSS 238
QY 130 DLPRGEFVVAIGSPFALONTVTTGTIVSTAQRGRELGLRSDMDYIQTDAIINNGSGP 189
Db 239 ELRPGEFVVAIGSPFALONTVTTGTIVSTAQRGRELGLRSDMDYIQTDAIINNGSGP 298
QY 190 LVNLGDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIYD--WKRFIGIRMTIT 246
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Db 299 LVNLGDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIYD--WKRFIGIRMTIT 358
QY 247 PSVLDELKASNPDPPEVSSGIYVOEVAPNSPSQSGIQQDGIYKNGRPLVDSSELQEA 306
Db 359 SSKAKELKDRHDFPDVIVSGAYITIEVPTPAEAGLKENVDIISINGQSVASANDVSDV 418
QY 307 VLTESPILLEVRGNDLFLSIAPEV 333
Db 419 IKRSTLMVVRGNDIMITVPEEI 445

RESULT 3
US-10-821-234-1465
; Sequence 1465, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labac, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PL SEQ_genes Version 1.0
; SEQ ID NO 1465
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1465

Query Match 61.6%; Score 1034.5; DB 6; Length 480;
Best Local Similarity 62.1%; Pred. No. 1.4e-80;
Matches 203; Conservative 60; Mismatches 55; Indels 9; Gaps 2;

QY 10 GLHQLSPRYKPNFADVVEKIAPAVVHIELFLRHPLEGRVNPVLSGSGFIMSEAGLIT 69
Db 158 GQEDPNSLRHKNFADVVEKIAPAVVHIELFLRHPLEGRVNPVLSGSGFIMSEAGLIT 217
QY 70 NAHVSSNSAAPGRQOLKVQLONGSDYEATIKDIDKSDIATIKIHPKKKLPLVLLGHSA 129
Db 218 NAHVVTN-----KRVVVELKNGATYEAKIKDVDEKADIALIKIDHGGKLVLLGRSS 271
QY 130 DLPRGEFVVAIGSPFALONTVTTGTIVSTAQRGRELGLRSDMDYIQTDAIINNGSGP 189
Db 272 ELRPGEFVVAIGSPFALONTVTTGTIVSTAQRGRELGLRSDMDYIQTDAIINNGSGP 331
QY 190 LVNLGDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIYD--WKRFIGIRMTIT 246
Db 332 LVNLGDEVIGINTLKTAGISFALPSDRITRFLTEFODKQIYD--WKRFIGIRMTIT 391
QY 247 PSVLDELKASNPDPPEVSSGIYVOEVAPNSPSQSGIQQDGIYKNGRPLVDSSELQEA 306
Db 392 SSKAKELKDRHDFPDVIVSGAYITIEVPTPAEAGLKENVDIISINGQSVASANDVSDV 451
QY 307 VLTESPILLEVRGNDLFLSIAPEV 333
Db 452 IKRSTLMVVRGNDIMITVPEEI 478

RESULT 4
US-11-183-914-11
; Sequence 11, Application US/11183914
; Publication No. US20050282214A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
```

```
APPLICANT: Tang, Tom Y.
APPLICANT: Shah, Puri
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/183,914
FILING DATE: 19-JULY-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mohan-Peterson, Sheila
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINITCT01
US-11-183-914-11

Query Match          52.5%; Score 882; DB 7; Length 458;
Best Local Similarity 52.5%; Pred. No. 1.3e-67;
Matches 169; Conservative 72; Mismatches 71; Indels 10; Gaps 2;
```

```
US-11-053-076-59
Sequence 59, Application US/11053076
Publication No. US20050255460A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Schweizer, Johannes
APPLICANT: Somoza Diaz-Sarmiento, Chamorro
APPLICANT: Belmares, Michael P.
TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
FILE REFERENCE: VITA-008CIP
CURRENT APPLICATION NUMBER: US/11/053,076
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: PCT/US03/28508
PRIOR FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/490,094
PRIOR FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: 60/450,464
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: 60/409,298
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 10/630,590
PRIOR FILING DATE: 2003-07-29
PRIOR APPLICATION NUMBER: 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/080,273
PRIOR FILING DATE: 2002-02-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ IDS: 330
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-11-053-076-59

Query Match          31.9%; Score 535; DB 7; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.7e-39;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 6
US-11-107-096-78
Sequence 78, Application US/11107096
Publication No. US20060003348A1
GENERAL INFORMATION:
APPLICANT: ZHANG, YINGNAN
APPLICANT: SIDHU, SACHDEV S.
TITLE OF INVENTION: CMT PDZ MODULATORS
FILE REFERENCE: P2100R1
CURRENT APPLICATION NUMBER: US/11/107,096
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 60/563,157
PRIOR FILING DATE: 2004-04-16
NUMBER OF SEQ IDS: 79
SEQ ID NO 78
LENGTH: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-11-107-096-78
```

Query Match	29.5%	Score 496;	DB 7;	Length 100;
Best Local Similarity	100.0%;	Pred. No. 1.1e-35;		
Matches 100;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Oy 235 KRFLGIRMRITTPSLVDLAKSNPDPEVSSGIYQVEAPNSPSQRGGIQDGLIVKNG 294
|||||
Db 1 KRFGLRMRITTPSLVDLAKSNPDPEVSSGIYQVEAPNSPSQRGGIQDGLIVKNG 60

QY	295	RPLVDSSELQEA	VL	T	S	P	L	L	E	V	R	G	N	D	L	L	F	S	I	A	E	V	M	334
Db	61	RPLVDSSELQEA	VL	T	S	P	L	L	E	V	R	G	N	D	L	L	F	S	I	A	E	V	M	100

```

RESULT 7
US-10-467-657-2096
? Sequence 2096, Application US/10467657
? Publication No. US20050260581A1
? GENERAL INFORMATION:
? APPLICANT: CITRON SpA
? APPLICANT: FONTANA Maria Rita
? APPLICANT: PIZZA Mariagrazia
? APPLICANT: MASTIGNANI Vega
? APPLICANT: MONACI Elisabetta
? TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
? FILE REFERENCE:
? CURRENT APPLICATION NUMBER: US/10/467,657
? CURRENT FILING DATE: 2003-08-11
? PRIOR APPLICATION NUMBER: GB-0103424.8
? PRIOR FILING DATE: 2001-02-12
? NUMBER OF SEQ ID NOS: 9218
? SOFTWARE: SeqWin99, version 1.04
? SEQ ID NO 2096
? LENGTH: 499
? TYPE: PRT
? ORGANISM: Neisseria gonorrhoeae
? US-10-467-657-2096

```

Query Match	24.7%;	Score 414;	DB 6;	Length 499;
Best Local Similarity	33.6%;	Pred. No. 1e-27;		
Matches 111; Conservative	58;	Mismatches 101;	Indels 60;	Gaps 9

```

Qy      25 ADVVEXKIAPVVHHELEFL-----HPLFGRRVP-----52
      58 AQLVQSGPVPVNIQAPAPRTONGSGNAETBDSPLABSDPPEYEFPKLVMPMPPIPOE 11
Db      53 -----LSGSGFTMSEAGLITTAHAVVSSNSAAPGRQQLVOLQNGDSYEATIKOIKKS 10
Qy      118 ADDGAGINFGSGFTIISKGYLLTNTHTVA-----GMSGIKVLNNKREYATLIGSDVQS 17
Db      108 DIATIKIHPKKKLPVLLIGHSADLRBPGEFVVAIGSPFALONTVYTGIVYTAQREGRGL 16
Qy      172 DVALKLKIDATEELPVAKIGNPKLKGEMVAALGAPFGDNSVTMGIVSA--KRSLLP- 22
Db      168 RDSMDMDYIQTDALINYNSGGPLVNLDEGYLTGINTLKT-----AGISFALPSDRITREL 22
Qy      228 NESYTFPIQTDVAINPNSGSGPLFNLKGQVGVGINSIQYRSGSGFMGIFSALPID-VANRV 28
Db      223 TEPEDDKQIKOMKKRPFGIIMRTITPSLVDELKASNPDPFVSSGGYVEVAANSPSORG 28
Qy      287 AE-OLKRTKGVKQRQLGVITIGEVSYGLAGSFGI-----DKASGALIAKILPGSFAERAG 33
Db      283 IQDDGIIVKVGRLVDSSELQEAIVTSP 312
Qy      340 LQAGDIYLSLDPGGEIRSSGDLPMVVAITP 369

```

RESULT 8
US-11-099-686-10591
; Sequence 10591, Application US/1109866
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.

```

; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098, 686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 10591
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10591

Query Match      24.4%   Score 410;   DB 7;   Length 474;
Beet Local Similarity 35.5%   Pred. No. 2.1e-27;
Matches 94; Conservative 58; Mismatches 89; Indels 24; Gaps 7

```

[illegible]

```

RESULT 9
US-10-454-437-56
Sequence 56, Application US/10454437
Publication No. US20050277115A1
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroege, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Hebehauser, Gregor
TITLE OF INVENTION: COMYNBACTERIUM GLUTAMINICUM GENES ENCODING PROTEINMS
TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPATION
FILE REFERENCE: BGI-128CPN
CURRENT APPLICATION NUMBER: US/10/454,437
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931636.8
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932127.2
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932129.9
PRIOR FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: DE 19932226.0
PRIOR FILING DATE: 1999-07-09

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PRIOR APPLICATION NUMBER: DE 19932920.6
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19932922.2
PRIOR FILING DATE: 1999-07-14
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO 56
LENGTH: 441
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-10-454-437-56

Query Match 21.5%; Score 360.5; DB 6; Length 441;
Best Local Similarity 34.5%; Pred. No. 3.2e-23;
Matches 101; Conservative 44; Mismatches 97; Indels 51; Gaps 9;

QY 27 VVKIAPVAVHIELFLRHPLEFGRNVLSSGSGFIMSEAGLITNAHVSSNSAARGQO- 85
DB 146 VAAAVLPVSVISQAIATR-----TSASBGSISISSDGYVTNNHVA-----GIBQS 192
QY 86 --LKVQLONGDSYEATIDIDKSDIATIKHPKKLPVLLGHADLRPFGEFVVAISGP 143
DB 193 GVLEVSFSDGTTAQADFIAGDSTDIAYIKIRDVSNLPVMSFGSDALGVQSVAAVAGSP 252
QY 144 FALQNTTGTGIVSTQREGREL--GLRDSMDYIQTDAIINNGSGPLVNLDEGVIGIN 201
DB 253 LGLSTVTGTGIVSAVNRPRASGDGESSLIDAIQTDAIINNGSGPLVMDGMLGMN 312
QY 202 TLKV-----TAGISFALPSDRITRFLTEPODKQIKDK--KRFIGIMRTITPSL 249
DB 313 SVIASISSTSDSAGSIGLGFISPSN----FAKRVADQLISTQVQPMIGVQVGT----- 363
QY 250 VDELKASNPDPPEVSSGIYQVEAPNSPQSGIGIDSGDIIVANKRPLVDSSE 302
DB 364 -----DNSVTGAVIASVODGPAADAGLQPGDGIYTKLNDR-VIDSPD 404

RESULT 10
US-11-074-176-4
Sequence 4, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: Altermann, Eric
APPLICANT: McAniff, Olivia
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: PaedSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 423
TYPE: PRT
ORGANISM: Lactobacillus acidophilus
US-11-074-176-4

Query Match 20.0%; Score 335.5; DB 7; Length 423;
Best Local Similarity 30.6%; Pred. No. 4e-21;
Matches 95; Conservative 54; Mismatches 114; Indels 47; Gaps 11;

QY 48 GRNVLSGSGGFIMSEA---GLITNAHVSSNSAARGQOLKQVLONGDSYEATIKD 104
DB 133 GLEETVSESSSVVWKSNGKGIYITNNHVTSSDA-----VQVQLANGKTVSAKVGKD 186
QY 105 KKSADIATIKHPKKLPVLLGHADLRPFGEFVVAIGSPFALO--NTVTTGIVSTQAR- 160
DB 187 STTDLAVSIDAKVYTGTAEPGDSKSLQAGGVIAVSGPLSGEYASTVYTGIIISAPRTI 246

QY 161 ---EGRELGLRDSMDYIQTDAIINNGSGPLVNLDEGVIGINTLKY-----TAGI 209
DB 247 STSSGNO-----QTVIQTDAIINPGNSGALVNSAQVIGINSMKLAQSDGTSVGM 299
QY 210 SFAIPSDRITRFLTEPODKQIKDK--KRFIGIR---MRTITPSLVDELKASNPDPPEVS 264
DB 300 GFALPSNEVTVINEL-----VKKGKTRPQGVAVALEGIPAVRSRLTKIS-----NLK 351
QY 265 SGIVQVEAPNSPQSGIGIDGIIVKNGRPLVDSSELQAVLVE---SPLEVERGN 321
DB 352 SGIVYASINKNSAANAMKSGDVITKVDGKVDVAVLSHLVSHKVDVTNITINNG 411
QY 322 DDLFESAPE 331
DB 412 RDVNLKVALR 421

RESULT 11
US-10-793-626-1824
Sequence 1824, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1824
LENGTH: 317
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1824

Query Match 18.9%; Score 318; DB 6; Length 317;
Best Local Similarity 31.9%; Pred. No. 8.1e-20;
Matches 86; Conservative 57; Mismatches 79; Indels 48; Gaps 11;

QY 56 GSGFI--MSB-AGLITNAHVSSNSAARGQOLKQVLONGDSYEATIKDIDKSDIAT 112
DB 27 GSGVLYQISEGSAYITNNHVD-----GASBIKQVQHNKQYDAKLGKDALTDIAYL 80
QY 113 KHPKKLPVLLGHADLRPFGEFVVAIGSPFALO--NTVTTGIVSTQAR- GRELGARD 169
DB 81 KIKDTKGKAIQFANSSVQGTGDSVFAANGNPLGEPANSVTSGTISASERTIDANTSAGN 140
QY 170 SMDYIQTDAIINNGSGPLVNLDEGVIGINTLKVTA---GISFALPSDRITRFLTEF 225
DB 141 TKAVNLQTDALINNGSGALVDINGNLVGNISKIAAQVGEIGFALPSNEVARTI--- 197
QY 226 QDKQIKDK--KRFIGIMRTITPSLVDELKASNPDPPE-----VSSGIYQVEAP 274
DB 198 -EQLVKHGKIRPISIGILINLS-----DIPENRKEIHTKDGKGVYAVK-- 242
QY 275 NSPQSGIGIDGIIVKNGRPLVDSSELQ 304
DB 243 ---DSENAIKKGIDITIGDKQIKDIDTDLR 269

RESULT 12
US-10-793-626-1832
Sequence 1832, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

Query Match	15.5%;	Score 260.5;	DB 6;	Length 493;
Best Local Similarity	27.2%;	Pred. No. 1,2e-14;		
Matches	75;	Mismatches	95;	Indels 43;
				Gaps 9

```

Qy      56 GSGFIHSEAG---LIITNHWYSSNAAAGROOLYOLONDSYEATIKIDKKSDIAT 112
Db      209 GSGVYVYKRVSDSYIYFNHAYVD-----QEKQVYTYGNDSKSYGVKVIQDKKMSDLAV 262
Qy      113 KIH-PKKLLPYLLGHSADLPGEFVAALGSPFA--LQNTYTTGYVYVAGHSEGLR- 168
Db      263 KAKVADENIKPMTGDSNNIKLAEPILIVIGNPLGTDFKSSQGVIS-----GLNR 313
Qy      169 -----DSDMDYIOTDAIINWYSSGGEPLVNLDEVIIGNTLKY---TAGISFA 212
Db      314 HVPVDIDKNDYDPLMAAFQIDAPVNPNGSSGAVVDROGRLLIGVSLKIDHNEGNAFA 373
Qy      213 IPSDRITFLTEFODKOIKDWKKRFFIGIRKKTTSBLYDELAKSNPDDP-EVSSGIYVOE 274
Db      374 IPINDVRKIAKELBHK-----GKVNYPNTETIKIKNVGLDSEKMININLPKVVHGVILGE 429
Qy      272 VAPNSPSSGGIIOGDPIIVKNGRPLVDSSELOAV 307
Db      430 VKENGLGRAGIUKGDYVIELDGKIDENLRHYQVI 465

```

```

RESULT 13
US-10-485-788A-774
; Sequence 774, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Carlick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 774
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-774

```

Query Match	15.5%	Score 259.5;	DB 6;	length 115;
Best Local Similarity	40.9%;	Pred. No. 1.8e-15;		
Matches 477	Conservative 34;	Mismatches 31;	Indels 3;	Gaps 1

RESULT 14
MS-11-053-076-152

```

? Sequence 152. Application US/11053076
? Publication No. US20050255460A1
? GENERAL INFORMATION:
? APPLICANT: Lu, Peter S.
? APPLICANT: Schweizer, Johannes
? APPLICANT: Somoza Diaz-Sarmiento, Chamorro
? APPLICANT: Belmares, Michael P.
? TITLE OF INVENTION: METHODS OF DIAGNOSING CERVICAL CANCER
? FILE REFERENCE: VITA-008CIP
? CURRENT APPLICATION NUMBER: US/11/053,076
? CURRENT FILING DATE: 2005-02-07
? PRIOR APPLICATION NUMBER: PCT/US03/28508
? PRIOR FILING DATE: 2003-09-09
? PRIOR APPLICATION NUMBER: 10/630,590
? PRIOR FILING DATE: 2003-07-29
? PRIOR APPLICATION NUMBER: 60/490,094
? PRIOR FILING DATE: 2003-07-25
? PRIOR APPLICATION NUMBER: 60/450,464
? PRIOR FILING DATE: 2003-02-27
? PRIOR APPLICATION NUMBER: 60/409,298
? PRIOR FILING DATE: 2002-09-09
? PRIOR APPLICATION NUMBER: 10/630,590
? PRIOR FILING DATE: 2003-07-29
? PRIOR APPLICATION NUMBER: PCT/US02/24655
? PRIOR FILING DATE: 2002-08-02
? PRIOR APPLICATION NUMBER: 60/309,841
? PRIOR FILING DATE: 2001-08-03
? PRIOR APPLICATION NUMBER: 60/360,061
? PRIOR FILING DATE: 2002-02-25
? PRIOR APPLICATION NUMBER: 10/080,273
? PRIOR FILING DATE: 2002-02-19
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 330
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 152
? LENGTH: 115
? TYPE: PRT
? ORGANISM: Homo sapiens
US-11-053-076-152

```

[illegible]

RESULT 15
US-11-107-096-77
Sequence 77, Application US/11107036
Publication No. US2006003348A1
GENERAL INFORMATION:
APPLICANT: SINDHU, SACHDEV S.
APPLICANT: ZHANG, YINGNAN
TITLE OF INVENTION: OMI PDZ MODULATORS
FILE REFERENCE: P210061

```

; CURRENT APPLICATION NUMBER: US/11/107,096
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 60/563,157
; PRIOR FILING DATE: 2004-04-16
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 77
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-107-096-77

```

```

Query Match 14.2%; Score 239; DB 7; Length 101;
Best Local Similarity 40.4%; Pred. No. 8.3e-14;
Matches 40; Conservative 32; Mismatches 27; Indels 0; Gaps 0;

```

```

Qy 235 KRFIGIRNRITTPSLVDELKASNPDPPEVSSGIYQEVAPNSPSQSGIODGDIIVKXNG 294
   1 KKYIGIRNMSLTSSKAKELKDRHRDPDVIGAYIIEVLPDPAPAGGKENDVITISNG 60
Qy 295 RPLVDSELQEAVALTESPILLLEVRGRNDLFSIAPEV 333
   61 QSVVSANDVSDVIKRESTIANVVRGRNEDIMITVIBEI 99
Db

```

Search completed: February 21, 2006, 21:16:43
 Job time : 19 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, **US-10-617-443B-2**Run on: February 21, 2006, 20:12:52 ; Search time 208 Seconds
(without alignments)
2854.354 Million cell updates/sec

Title: US-10-617-443B-2

Perfect score: 1679
Sequence: 1 MHLLPASPAGHQLSSPRK.....LEVRGNDLLFSAPEVVM 334

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODL=frim+p2n.model -DEV=xlp
-Q=/abs/ABSSWB.epool/US10617443/runat_21022006.165823.17255/app_query.fasta_1
-DB=Issued Patents NA -QPMT=fastac -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODS=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs803p -USER=US10617443@cgn_1_1_290@runat_21022006.165823.17255
-NCPU=6 -ICPU=3 -NO MWAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=130 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1034.5	61.6	1521	3	US-09-949-016-4643 Sequence 4643, App
2	1034.5	61.6	1894	3	US-10-104-047-795 Sequence 795, App
3	1034.5	61.6	2036	3	US-09-949-016-139 Sequence 399, App
4	1034.5	61.6	2205	3	US-08-888-077A-41 Sequence 41, App
5	1027.5	61.2	2036	3	US-08-923-454A-17 Sequence 17, App
6	920	54.8	1859	3	US-09-724-864-22 Sequence 22, App
7	882	52.5	1835	3	US-08-923-454A-7 Sequence 7, App
8	882	52.5	2040	3	US-09-075-460-4 Sequence 4, App
9	882	52.5	2187	3	US-08-923-454A-23 Sequence 23, App

10	882	52.5	2187	3	US-08-923-454A-24	Sequence 24, Appl
11	882	52.5	2476	3	US-09-008-271A-23	Sequence 23, Appl
12	882	52.5	2476	3	US-09-966-415-23	Sequence 23, Appl
13	878	52.3	2187	3	US-08-923-454A-30	Sequence 30, Appl
14	834.5	49.7	1787	3	US-08-923-454A-3	Sequence 3, Appl
15	834.5	49.7	2551	3	US-08-923-454A-26	Sequence 26, Appl
16	779	46.4	1503	3	US-08-923-454A-5	Sequence 5, Appl
17	779	46.4	2144	3	US-08-923-454A-28	Sequence 28, Appl
18	579.5	34.5	539	2	US-08-322-742-18	Sequence 18, Appl
19	454	27.0	1230230	3	US-09-438-185A-1	Sequence 1, Appl
20	450.5	26.8	1425	3	US-09-489-039A-6523	Sequence 6523, Ap
21	444	26.4	1332	3	US-09-902-540-4672	Sequence 4672, Ap
22	444	26.4	24754	3	US-09-902-540-1230	Sequence 1230, Ap
23	441.5	26.3	1368	3	US-09-711-164-245	Sequence 245, Ap
24	437	26.0	1386	3	US-09-902-540-4598	Sequence 4598, Ap
25	437	26.0	27707	3	US-09-902-540-1226	Sequence 1226, Ap
26	431	25.7	1068	3	US-09-711-164-246	Sequence 246, Ap
27	430	25.6	1230025	3	US-09-198-452A-1	Sequence 1, Appl
28	428	25.5	1436	3	US-09-199-637A-131	Sequence 131, App
29	425	25.3	1428	3	US-09-252-991A-12923	Sequence 12923, A
30	425	25.3	1455	3	US-09-252-991A-12561	Sequence 12561, A
31	424	25.3	732	3	US-08-923-454A-1	Sequence 1, Appl
32	422	25.1	1980	2	US-08-350-741-1	Sequence 1, Appl
33	422	25.1	1980	2	US-08-463-875A-1	Sequence 1, Appl
34	418	24.9	1500	3	US-09-673-898-5	Sequence 5, Appl
35	417	24.8	1083	3	US-09-489-039A-6463	Sequence 6463, Ap
36	415	24.7	1110	3	US-09-673-898-7	Sequence 7, Appl
37	414	24.7	1242	3	US-09-388-090-5	Sequence 5, Appl
38	414	24.7	1326	3	US-09-388-089B-13	Sequence 13, Appl
39	414	24.7	1395	3	US-09-388-089B-10	Sequence 10, Appl
40	414	24.7	1395	3	US-09-388-090-3	Sequence 3, Appl
41	414	24.7	1611	2	US-08-485-569-1	Sequence 1, Appl
42	414	24.7	1611	2	US-08-480-993-1	Sequence 1, Appl
43	414	24.7	1611	2	US-07-903-079B-1	Sequence 1, Appl
44	413	24.6	1830121	3	US-09-557-884-1	Sequence 1, Appl
45	413	24.6	1830121	3	US-09-643-990A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-4643
; Sequence 4643, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4643
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4643

Alignment Scores:

Pred. No.:	7,276-111	Length:	1521
Score:	1034.50	Matches:	203
Percent Similarity:	80.4%	Conservative:	60
Best Local Similarity:	62.1%	Mismatches:	55
Query Match:	61.6%	Indels:	9
DB:	3	Gaps:	2

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US-10-617-443B-2 (1-334) x US-09-949-016-4643 (1-1521)

Qy 10 GlyLeuHisGlnLeuSerSerProArgTyrTyrPheAsnPhelIleAlaAspValValGlu 29
Db 2 GGGGAGGAGATCCCAACAGTTTGGCCAAATAATATTAATTTTCGGGAGCGTGGAG 61
Qy 30 LysIleAlaProAlaValAlaHisIleGlnLeuPheLeuArgHisProLeuPheGlyArg 49
Db 62 AAGATGCGCCCTGCGCGTTCATATGCAATTTGTTTGGCAAGCTTCCGTTTCTAAACGA 121
Qy 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGlnAlaGlyLeuIleIleThr 69
Db 122 GAGGTGCGCGTGGCTAGTGCGGTCTGGGTTTATTTGTCGGAAGATGCAATGATCGAGCA 181
Qy 70 AsnAlaHisValAlaSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGln 89
Db 182 AATGCGCCAGTGGAGCAAC-----AAGCAACGGGCTCAAAAGTTGAG 223
Qy 90 LeuGlnAsnGlyAspSerTyrGlyAlaAlaThrIleLysAspIleAspLysSerAspIle 109
Db 224 CTGAAGACGGTCCCACTTCGAAAGCCAAATACAGATGTGATGAGAAAGCAGACATC 283
Qy 110 AlaThrIleLysIleHisProLysLysLeuProValLeuLeuGlyHisSerAla 129
Db 284 GCACGTATCAAAATTGACCAAGGCGCAAGCTGCTGCTGCTGGCGCTCTCTCA 343
Qy 130 AspLeuArgProGlyGluPheValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 344 GACCTGGGCGGGAGAGTTCGTGGTCCATCGAAAGCCCGTTTCCCTCAAAACAA 403
Qy 150 ValThrThrGlyIleValSerThrAlaGlnArgGlyArgGlyLeuGlyLeuArgAsp 169
Db 404 GTCACACCGGGATTCGTGAGCACACCCAGCGAGGGGCAAAAGCTGGGGGCTCCGCAAC 463
Qy 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro 189
Db 464 TCAGACATGACATCACTCCAGACGACGCGCATCATCACTATGAACTCGGGAGGCGCG 523
Qy 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuValThrAlaGlyIle 209
Db 524 TTGATTAACCTGACGAGTGAAGTGAATTTGAATTAACCTTTGAAATGACAGCTGGAATC 583
Qy 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspGln 229
Db 584 TCCTTTGCATCCCATCTGATTAAGATTAATAAAGTTCTCTCCAGGAGTCCCATGACGAG 643
Qy 230 IleLysAsp-----TrpLysLysArgPheIleGlyIleArgMetArgThrIleThr 246
Db 644 GCCAAAGGAAAGCCATCACCAAGAAAGATATTTGATTCGAATGATGTCACATCACG 703
Qy 247 ProSerLeuValAspGlyLeuLysValSerAsnProAspPheProGlyValSerSerGly 266
Db 704 TCCAGCAAGCCAAAGAGCTGAAAGACCGGACCGGAACTTCCAGACGTGATCTCAGAA 763
Qy 267 IleTyrValGlnGluValAlaProAsnSerProSerGlnArgGlyGlyIleGlnAspGly 286
Db 764 GGGTATATATGAAGTAATTCCTGATACCCCGAGAGCTGGTGTCTCAAGAAAC 823
Qy 287 AspIleIleValLysValAsnGlyArgProLeuValAspSerSerGlnLeuGlnAla 306
Db 824 GACGTATATATGACATCAATGACAGTCCGTGGTCTCCGCAATGATTCAGCGAGCTC 883
Qy 307 ValLeuThrGluSerProLeuLeuGlnValAlaArgArgGlyAsnAspAspLeuPhe 326
Db 884 ATTTAAAGGAAAGCAGCTGAAACGTGTGTCGAGGGGTAAAGATATCATGATC 943
Qy 327 SerIleAlaProGlyValVal 333
Db 944 ACAGTGATTCGGAAGAAATT 964

RESULT 2
US-10-104-047-795
; Sequence 795, Application US/10104047.
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; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241e1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 795
; LENGTH: 1894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-795

Alignment Scores:
Pred. No.: 1,02e-110 Length: 1894
Score: 1034.50 Matches: 206
Percent Similarity: 80.28 Conservative: 61
Best Local Similarity: 61.98 Mismatch: 57
Query Match: 61.64 Indels: 10
DB: Gaps: 2

US-10-617-443B-2 (1-334) x US-10-104-047-795 (1-1894)

Qy 4 AlaLeuProAlaSerAlaGlyLeuHisGlnLeuSerSerProArgTyrTyrPheAsnPh 23
Db 358 GCGGAGCCTCGGCGCAAGCGCAG-GAAGATCCCAAGTTTGGCCCATTAATTAATCTTT 416
Qy 24 IleAlaAspValValGluValIleAlaProAlaValAlaHisIleGlnLeuPheLeuArg 43
Db 417 ATCGGAGCGTGGTGAAGAAATGCCCCCTCCGTTGTTCAATGAAATTTTTCGCAAG 476
Qy 44 HisProLeuPheGlyArgAsnValProLeuSerSerGlySerGlyPheIleMetSerGlu 63
Db 477 CTTCGTTTTCAAACAGAGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
Qy 64 AlaGlyLeuIleIleThrAsnAlaHisValAlaSerSerAsnSerAlaAlaProGlyArg 83
Db 537 GATGACATGATCGTGAACAAATGCCCCACGTGTCACCA-----AAG 578
Qy 84 GlnGlnLeuValGlnLeuGlnAsnGlyAspSerTyrGlyAlaThrIleLysAspIle 103
Db 579 CACCGGATCAAGTTGACCTGAAGACGCTCCCTTACGAAAGCCAAATTAAGGATGTG 638
Qy 104 AspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLeuProValLeu 123
Db 639 GATGAAAGCAGACATCGCATCAATTAATTCACCAAGGCAAGCTGCTGCTG 698
Qy 124 LeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValAlaIleGlySerPro 143
Db 699 CTGCTGGCCGCTCTCGAGACTCGGCGGGAAGTTCGTGTCGCATCGAAGCCG 758
Qy 144 PheAlaLeuGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArgGlyArg 163
Db 759 TTTTCCCTTCAAAACAGATGACACCGGATCTGTGACACACCCAGCGAGGCGCA 818
Qy 164 GluLeuGlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyr 183
Db 819 GAGCTGGGGCTCCGCACTCAGACATGACATCAATCCAGACCGCATCATCACTAT 878
Qy 184 GlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeu 203
Db 879 GAAACTCGGAGGCGCGTTAGTAACCTGACGTAAGATGGAATTAATTAACATTTG 938
Qy 204 LysValThrAlaGlyLysSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
Db 939 AAGTGACAGCTGAATCTCTTTGCATCCCATCTATTAAGATTAATAAAGTTCTCTCAG 998
Qy 224 GluPheGlnAspLysGlnIleLysAsp-----TrpLysLysArgPheIleGlyIle 240
Db 224 GluPheGlnAspLysGlnIleLysAsp-----TrpLysLysArgPheIleGlyIle 240
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/888,077A
/ FILING DATE: 03-JUL-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/592,541
/ FILING DATE: 26-JAN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: PALISI, THOMAS M
/ REGISTRATION NUMBER: 36,629
/ REFERENCE/DOCKET NUMBER: SCHERING 3.0-017 CIP CIP IV
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (908) 654-5000
/ TELEFAX: (908) 654-7866
/ INFORMATION FOR SEQ ID NO: 41:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2205 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: 1..2205
/ OTHER INFORMATION: /note="multim1-TW2"
US-08-888-077A-41

Alignment Scores:
Pred. No.: 1,29e-110 Length: 2205
Score: 1034.50 Matches: 206
Percent Similarity: 80.2% Conservative: 61
Best Local Similarity: 61.9% Mismatches: 57
Query Match: 61.6% Indels: 10
DB: Gaps: 2

US-10-617-443B-2 (1-334) x US-08-888-077A-41 (1-2205)
QY 4 A1aleuProAlaserlAgileuH1sgInleuSerSerProArgrTyrIleuPheanphe 23
DB 579 GGGAGCCCTGGCGCCAAAGGCGAG-GAAGATCCCAACAGTTTGCGCATTAATTAACCTT 637
QY 24 l1ealaSpValaValaGluYsIlealaProAlaValaH1sIleGluIleuPheuaarg 43
DB 638 ATCGCGAGAGTGGTGAAGAAAGATCGCCCGCTGTTCAATTCGAATTGTTGGCAAG 697
QY 44 H1sProIleuPheGlyArGAnValProIleuSerSerGlySerGlyPheIleuMetSerGlu 63
DB 698 CTTCCTTTTCTTAAACGAGAGCGTGGCGCTGCTGGCTTTTATTGTGTGGAA 757
QY 64 A1aGlyLeuIleIleThraHnAlaH1sValIleSerSerAnSerAlaIaProGlyarg 83
DB 758 GATGACTATCTGTGCAAAATGCGCACGTGTGATCAAC-----AAG 799
QY 84 GInGInleuYsValGInleuGInAnGlyAspSerTyrGluAlaThrIleYsAple 103
DB 800 CACCGGCTCAAGATTAGCTGAAGAAAGCGGTGCCACTTACGAAGCCAAATCAAGATGCG 859
QY 104 AapYsYsSerAspIleAlaThrIleYsIleH1sProIleYsYsYsLeuProValleu 123
DB 860 GATGAGAAAGCAGACTCCACACTCATCAAAATTGACCCAGGGGAGCTGCTGTCCG 919
QY 124 LeuIleuGlyH1sSerAlaApleuAargProGlyGluPheValaIaIleGlySerPro 143
DB 920 CTGCTTGCGCTCTCTCAAGCTGCGCGGAGAGATTGTGTGCTCCATCGGAAGCCCG 979
QY 144 PheAlaIleuGInAnSerValaThrThrGlyIleValaSerThrAlaInArgGluYarg 163
DB 980 TTTTCCCTCAAAACACAGTCAACCAACCGGATGTGTAGACACCAACGAGGAGCGGCAAA 1039
QY 164 GluIleuGlyLeuArGAspSerAspMetAspTyrIleGInThrAspAlaIleIleAnTyr 183
DB 1040 GAGCTGGGGCTCGCAATCAGACATGACTATCATCCAGACGACCCATCATCAACTAT 1099
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QY 184 GlyAnSerGlyGlyProIleuValaAnleuAspGlyGluValIleGlyIleAnThrIleu 203
DB 1100 GGAACCTGGAGGCGCCCTGTAGTAACCTGACGCTGAAGCATTTGAATTAACCTTGG 1159
QY 204 lYsValIleAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheIleThr 223
DB 1160 AAAGTACAGCTGGAATCTCTTTCATCCATCCATCTGAATTAAGTAAAGATTCTCCACG 1219
QY 224 GluPheGInAapYsGInIleYsAsp-----TrrYsYsYsArgPheIleGlyIle 240
DB 1220 GATGCCATGACCGCAGAGCCCAAGAAAAGCATCACCAAGAAAAGTATATTTGTATC 1279
QY 241 ArgMeArGTrIleThrProSerIleuValaAspGluYsAlaSerAspProAspPhe 260
DB 1280 CGAATGATGTCTACCTACCTCCAGCAAAACCAAGAGCTGAAGAGACCGGACCGGACTTC 1339
QY 261 ProGluValaSerSerGlyIleTyrValaGInGluValaIaProAnSerProSerGInArg 280
DB 1340 CCAGACGTGATCTCAGAGCGTATATTAATTAAGTAATTCCTGATTAACCCAGAGAGCT 1399
QY 281 GlyGlyIleGInAspGlyAspIleIleValaYsValaAnGlyArGProIleuValaAspSer 300
DB 1400 GGTGTCTCAAGAAACGACGTCTATATCAAGCATCAATGACAGTCCGTGTCTCCGCC 1459
QY 301 SerGluIleuGInGluAlaValleuThrGluSerProIleuLeuGluValaArgArgGly 320
DB 1460 AATGATGTCAAGGAGCTCATTAATAAGGAAAGACCCCTGAACATGTGTCTCCGAGGCT 1519
QY 321 AanaAspAspLeuIleuPheSerIleAlaProGluValaI 333
DB 1520 AATGAAGATATCATGATCAAGTGAATTCGCAAGAAAT 1558

RESULT 5
US-08-923-454A-17
/ Sequence 17, Application US/08923454A
/ Patent No. 6004794
/ GENERAL INFORMATION:
/ APPLICANT: Creasy, Caretha
/ APPLICANT: Livi, George
/ APPLICANT: Karlan, Eric
/ APPLICANT: Clinkdeard, Helen
/ APPLICANT: Browne, Michael
/ APPLICANT: Southan, Christopher
/ TITLE OF INVENTION: HUMAN SERINE PROTEASE
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SmithKline Beecham Corporation
/ STREET: 709 Swedeland Road
/ CITY: King of Prussia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19406
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/923,454A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/025436
/ FILING DATE: 06-SEPT-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Baumeister, Kirk
/ REGISTRATION NUMBER: 33,833
/ REFERENCE/DOCKET NUMBER: P50547
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-5096
/ TELEFAX: 610-270-5090
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2036 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-923-454A-17 Feature polymorphism at 1325

Alignment Scores:
Pred. No.: 7,496-110 Length: 2036
Score: 1027.50 Matches: 205
Percent Similarity: 79.94 Conservative: 61
Best Local Similarity: 61.64 Mismatches: 58
Query Match: 61.24 Indels: 10
DB: 3 Gaps: 2

US-10-617-443B-2 (1-334) x US-08-923-454A-17 (1-2036)

QY 4 AlaLeuProAlaSerAlaGlyLeuH1eG1LeuSerSerProArgTyrLysPheAsnPhe 23
DB 503 GCGAGCCTCGCGGCGCAAGCGCAG-GAAGATCCCAACAGTTGCGCATTAATTAACATT 561
QY 24 IleAlaSerValAlaGlyLeuIleAlaProAlaValAlaH1eG1LeuPheLeuArg 43
DB 562 ATCCGCGAGCGTGTGAGAAAGATGCGCCCTGCGGTTCATATGAAATTGTTGGCAG 621
QY 44 HisProLeuPheGlyArgAsnValProLeuSerSerGlySerGlyPheIleMetSerGlu 63
DB 622 CTTCGTTTCTTAAACGAGAGGTCGCGGTGCTAGTGGTTCGCGTTATTGTCGCGAA 681
QY 64 AlaGlyLeuIleIleThrAsnAlaHisValAlaSerSerAsnSerAlaAlaProGlyArg 83
DB 682 GATGACTGATCGTACAAATGCCCCAGCTGGTACCAAC-----AAG 723
QY 84 G1nG1nLeuLysValG1nLeuG1nAsnG1nLysSerTyrG1uAlaThrIleLysAspIle 103
DB 724 CACCGGCTCAAAAGTTGACTGAAGACGCTGCCACTTCGAAAGCCAAATCAAGATGTG 783
QY 104 AspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLeuProValLeu 123
DB 784 GATGAAAGACGACATCGCACTCAAAATTGACCAACAGGCGCAAGCTGCTGCTCG 843
QY 124 LeuLeuG1HisSerAlaAspLeuArgProG1uG1uPheValAlaAlaIleG1LysSerPro 143
DB 844 CTGCTTGCCCTCTCAGAGCTGCGGCGGAGAGTTGCTGTGCCATCGGAACCCG 903
QY 144 PheAlaLeuG1nAsnThrValThrThrG1LysIleAlaSerThrAlaG1nArgG1uLysArg 163
DB 904 TTTTCCCTTCAAAACACAGTCCACCGGATCGTGAACACACACCGAGCGGCGCAA 963
QY 164 G1uLeuG1LysLeuArgSerAspSerAspIleTyrIleG1nThrAspAlaIleIleAsnTyr 183
DB 964 GAGCTGGGCTCCGCACTCAGACATGCACTACATCCAGACCGCATCATCAACTAT 1023
QY 184 G1LysAsnSerG1G1LysProLeuValAsnLeuAspG1uG1uAlaIleG1LysAsnThrLeu 203
DB 1024 GGAACCTGGAGGCGCGCTTGAATTAACCTGAGCGGTGAAGTGAATTGAATTAACTTGG 1083
QY 204 LysValThrAlaG1LysSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
DB 1084 AAAGGACAGCTGGAATCTCTTTCATCCCATCTGATTAAGATTAAAGTTCTCTCAG 1143
QY 224 G1uPheG1nAspLysG1nIleLysAsp-----TrrLysLysArgPheIleG1Lys 240
DB 1144 GAGTCCCATGACGAGCGCAAGAAAGCCATCAACCAAGAAAGATATTGTGTATTC 1203
QY 241 ArgMetArgThrIleThrProSerLeuValAspG1uLeuLysAlaSerAsnProAspPhe 260

DB 1204 CGAATGATCATCTACCTCCAGCAAGCCAAAGAGCTGAAGAGACCGGACCTTC 1263
QY 261 ProG1uValSerSerGlyIleTyrValG1nG1uValAlaProAsnSerProSerG1nArg 280
DB 1264 CCAAGCGTATCTCAGAGCGGTATATTAATTAAGTAATTCCTGATACCCAGAGAAAGCT 1323
QY 281 G1yG1LysIleG1nAspG1LysAspIleIleValLysValAsnG1LysArgProLeuValAspSer 300
DB 1324 GKTGCTCAAGAAACGAGCTCATATATCATCAATGAGACAGTCCGTGCTCCGCC 1383
QY 301 SerG1uLeuG1nG1uAlaValLeuThrG1uSerProLeuLeuG1uValArgArgG1Lys 320
DB 1384 AATGATGCACCGACGCTATTAAAGGAAAGCACCCCTGAACATGCTGTCCGAGGGGT 1443
QY 321 AsnAspAspLeuLeuPheSerIleAlaProG1uValVal 333
DB 1444 AATGAAGATATCATGATCAGATGATCCCGAAGAAATT 1482

RESULT 6
US-09-724-864-22
Sequence 22, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724, 864
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 1859
TYPE: DNA
ORGANISM: Mouse
US-09-724-864-22

Alignment Scores:
Pred. No.: 2,436-97 Length: 1859
Score: 920.00 Matches: 191
Percent Similarity: 67.04 Conservative: 67
Best Local Similarity: 49.64 Mismatches: 66
Query Match: 54.84 Indels: 61
DB: 3 Gaps: 4

US-10-617-443B-2 (1-334) x US-09-724-864-22 (1-1859)

QY 4 AlaLeuProAla-----SerAlaGlyLeuH1eG1nLeu 14
DB 63 GCGCTCCCGCTGTGCGCAGTGCAGAAAGGCTCTGCGAAGAGCGGAGCAACAAAGACA 122
QY 15 SerSerProAlaG1LysPheAsnPheIleAlaAspValAlaG1uValIleAlaProAla 34
DB 123 GCGCGGCTCCGGAAGAAAGTACACTTCGCGCAGGTGTGAGAAAGTGCGCGCTCT 182
QY 35 ValValHisIleG1LeuPheLeuArg----- 43
DB 183 GTGCTCCACTTCAGAGCTTTCGAGATGACAGACACAGGTTCCCACTGATCTTAA 242
QY 43 ----- 43
DB 243 GAGAGACACCATCTGGAACCCAGATCTCAGTTGTTCGAAAGATGCGCCAGAGCA 302
QY 44 -----HisProLeuPheG1LysArgAsnValArg 52
DB 303 GCTTCAGGCACTCAAAAGACATGGAATGATCACTTCCCAACGAAATATCC 362
QY 52 OLeuSerSerG1LysSerGlyPheIleMetSerG1uAlaG1LysLeuIleIleThrAsnAlaH1 72

```

STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PaateSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923.454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURES:
NAME/KEY: Coding Sequence
LOCATION: 251...1624
OTHER INFORMATION:
US-08-923-454A-7

Alignment Scores:
Pred. No.:      6.61e-93      Length:      1835
Score:          882.00       Matches:     169
Percent Similarity: 74.8%   Conservative: 72
Best Local Similarity: 52.5% MisMatches:  71
Query Match:    52.5%      Indels:     10
DB:             3          Gaps:        2

US-10-617-443B-2 (1-334) x US-08-923-454A-7 (1-1835)

Oy      15 SerSerProArTyRlyephehaphel1ea1aaapVala1glulysilealapaola 34
Db      671 GCCTTCGCCCGAGACGACAGCAACTTCCATCCAGATGTGGTGGAAGAAGACAGCATGC 730
Oy      35 ValValHle1legluleuPheleuArgh1aProleuehgiArghaenVal1Proleuse 54
Db      731 GTGGCTAAATCCAGATCCCTGGACCAGCACCCCTTTCTGGGCCCGCAGAGCTCTATCTCG 790
Oy      55 Ser1yGer1yPhel1ewetserg1unagiyleu1le1ethraema1ah1eva1val 74
Db      791 AACGAGCTCAGAGATTCGTGGTGGCTGCCGATGGGCTCATTTGCACCAACGCCCATGTGGTG 850
Oy      75 SerSerAnseRalalaPaProglyArGInginleu1yVal1GlnleuGlnAanG1yAp 94
Db      851 GGTGAT-----CGGCGCAGAGTCCGTGTGAAGACTGCTTAAGCGCGCAC 892
Oy      95 SerTyrglu1aThr1leySaer1leaapLy1ySerarPl1ealTh1le1y1le 114
Db      893 AGG1ATGAGGCGCGTGTGCACAGCTGTGATCCCGTGGCGACATCGAACCGCTAAGGATT 953
Oy      115 HlaProLy1y1yLeuProVal1leu1leuG1yH1aSerAla1aapLeuArProGly 134

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Db      953 CAGACTAAGAGACCTCTCCCAACGCTGCTGGAGACGTCAGTCGATGTCGGAGAGG 1012
Qy      135 GtupheValAlaIleGlySerProPheAlaLeuGlnAenThrValThrThyIle 154
Db      1013 GAGTTGTGTGGTCAGGGAAGTCCCTTGGACATCGAAGAACATGATCAATCCGGCATT 1072
Qy      155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuAArgAspSerAspMetAspTyr 174
Db      1073 GTTACCTCTGCTCGACGCTCCAGCCAGACCTGGAGATCCCCCAACCAATGTGAATAC 1132
Qy      175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
Db      1133 ATTCAAATGATGACGATTCATTGATTTTGAACCTGTGAGATGCCCTGTTAACTTGAT 1192
Qy      195 GlyGluValIleGlyIleAsnThrLeuValThraGlyIleSerPheAlaIlePro 214
Db      1193 GGGAGGTGATGTGAGTGAACACATGAAGTCAAGCTGGAATCTCTTCCATCCCT 1252
Qy      215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspIleGln-----Ile 230
Db      1253 TCTGATCGCTTCGAGAGTTCTGCACTGGGGAAAGAAAGAAATTCCTCTCCGGAATC 1312
Qy      231 LysAspTrpLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
Db      1313 AGTGGTCCCAAGCGCGCTACATTTGGGGATGATGATCCCTGATCCCAAGCATCTT 1372
Qy      251 AspGluLeuValAsnSerAspAspPheProGluValSerSerGlyIleTyrValGln 270
Db      1373 GCTGAATCTACAGCTTCGAGAACCAAGCTTCCGATGTTCCAGCATGATGATCATCAT 1432
Qy      271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
Db      1433 AAAGTCATCTGGGCTCCCTCGACACCGGGCTGCTCGGGCTGGATGTGATTTTG 1492
Qy      291 LysValAsnGlyArgProLeuValAspSerSerGlnGluAlaValLeuThrglu 310
Db      1493 GCCATTGGGAGCAATGTTACAAATGCTGAAGATGTTATGAAGCTTTGAAACCCA 1552
Qy      311 SerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaPro 330
Db      1553 TCCCAATGTCAGTCAGATCCGGCGGGGACGAGAAACACTGACCTTATATGTACCCCT 1612
Qy      331 GluVal 332
Db      1613 GAGGTC 1618

RESULT 8
US-09-075-460-4
; Sequence 4, Application US/09075460A
; Patent No. 6489136
; GENERAL INFORMATION:
; APPLICANT: Zervos, Antonio S.
; TITLE OF INVENTION: CELL PROLIFERATION RELATED GENES
; FILE REFERENCE: 10284/004001
; CURRENT APPLICATION NUMBER: US/09/075,460A
; CURRENT FILING DATE: 1998-05-08
; EARLIER APPLICATION NUMBER: US 60/046,077
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (248) .. (1834)
US-09-075-460-4

Alignment Scores:
Pred. No.: 7,77e-93 Length: 2040
Score: 882.00 Matches: 169

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Percent Similarity: 74.8% Conservative: 72
Best Local Similarity: 52.5% Mismatches: 71
Query Match: 52.5% Indels: 10
Db: 3 Gaps: 2

US-10-617-443b-2 (1-334) x US-09-075-460-4 (1-2040)
Qy      15 SerSerProArgTyrLysPheAsnPheIleAlaAspValIleGluValIleAlaProAla 34
Db      861 GCTTCTCCCGAGTCAGTACACTTCATCCGAGATGGGGAGAGAACACACACTCTCC 940
Qy      35 ValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
Db      941 GTGCTATATCGAGATCTCGACCGGACCTTTCTTGGCCGGAGATCCCTATCTCG 1000
Qy      55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValVal 74
Db      1001 AACGGCTCAGGATTCGTGGTGGCTGCCATGGGCTCATGTGCACCAACGCCCATGTGTG 1060
Qy      75 SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAsp 94
Db      1061 GCTGAT-----CGGCGCAGAGTCCGTGAGACTCTTAAGCGGCAAC 1102
Qy      95 SerTyrGluAlaThrIleLysAspIleAspLysSerAspIleAlaThrIleLysIle 114
Db      1103 ACGTATAGGCGCGGTGTCACAGCTGTGATCCCGTGGCAGACATCGCAACGTCAGATT 1162
Qy      115 HisProLysLysLysLeuProValLeuLeuGlnGlyHisSerAlaAspLeuArgProGly 134
Db      1163 CAGACTAAGAGCCCTCTCCACGCTGCTGGGACCTCAGCTGATGTCCGGCAAGG 1222
Qy      135 GluPheValAlaAlaIleGlySerProPheAlaLeuGlnAenThrValThrThyIle 154
Db      1223 GAGTTGTGTGGTCATGGAGATCCCTTTCATGCACTGCAAGAACATCATCATCCGGCATT 1282
Qy      155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuAArgAspSerAspMetAspTyr 174
Db      1283 GTTACCTCTGCTCGACGCTCCAGCCAGACACTGGGACTCCCAACCAAGTGAATAC 1342
Qy      175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
Db      1343 ATTCAAATGATGACGATTCATGATTTGGAACCTCGAGAGTCCCTGTGTAACTTGAT 1402
Qy      195 GlyGluValIleGlyIleAsnThrLeuValThraGlyIleSerPheAlaIlePro 214
Db      1403 GGGAGGTGATGTGAGTGAACACATGAAGTCAAGCTGAATCTCTTGGCATCCCT 1462
Qy      215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspIleGln-----Ile 230
Db      1463 TCTGATCGCTTCGAGAGTTCTGCACTGTGGGAAAGAAAGAAATTCCTCTCCGGAATC 1522
Qy      231 LysAspTrpLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
Db      1523 AGTGGTCCCAAGCGCGCTACATTTGGGGATGATGTCGACCCCTGAGTCCCAAGCATCTT 1582
Qy      251 AspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrValGln 270
Db      1583 GCTGAATCTACAGCTTCGAGAACCAAGCTTCCCAATGTTCAAGCATGTGATCTCATCAT 1642
Qy      271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
Db      1643 AAAGTCATCTGGGCTCCCTCGACACCGGGCTGCTCGGGCTGGATGTGATTTTG 1702
Qy      291 LysValAsnGlyArgProLeuValAspSerSerGlyGlnGluAlaValLeuThrglu 310
Db      1703 GCCATTGGGAGCAGATGTTCAAAATGCTGAAGATGTTTGAAGCTGTTGAAACCCA 1762
Qy      311 SerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaPro 330
Db      1763 TCCCAATGTCAGTCAGATCCGGCGGGGACGAGAAACACTGACCTTATATGTACCCCT 1822
Qy      331 GluVal 332

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DB 1823 GAGTTC 1828

RESULT 9

US-08-923-454A-23
Sequence 23, Application US/08923454A
Patent No. 6004794

GENERAL INFORMATION:

APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karian, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923.454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090

TELEX:

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 2187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 603..1976
OTHER INFORMATION:
US-08-923-454A-23

Alignment Scores:

Prod. No.: 8.65e-93 Length: 2187
Score: 882.00 Matches: 169
Percent Similarity: 74.8% Conservative: 72
Best Local Similarity: 52.5% Mismatches: 71
Query Match: 52.5% Indels: 10
Gaps: 2

US-10-617-443B-2 (1-334) x US-08-923-454A-23 (1-2187)

DB 1023 GCTTCTCCCGAGTCACTGACATTGATGCTGTGAGAAAGACAGCAGCTGCTC
15 SerSerProLeuArgTyrIleValPheAsnProIleAlaAspValValGluIleValIleAlaProIle 34
DB 1023 GCTTCTCCCGAGTCACTGACATTGATGCTGTGAGAAAGACAGCAGCTGCTC 1082

QY 35 ValValIleHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
DB 1083 GTGGTCTATATGAGATCTGAGCCGACCTCTTTCTGGCCCGGAGGTCCTCATCTCG 1142
QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValVal 74
DB 1143 AACGGCTCAGATTGGTGTGCTGCCGATGGGCTCATTTGTCACACAGCCCATGTGCTG 1202
QY 75 SerSerAsnSerAlaAlaProGlyArgGlnGluLeuValGluLeuGluAsnGlyAsp 94
DB 1203 GCTGAT-----CGGCGAGAGTCCGTGTAGACTCTAAGCGCGAC 1244
QY 95 SerTyrGluAlaThrIleLeuAspIleAspLysLysSerAspIleAlaThrIleLeuIle 114
DB 1245 ACGTATGAGCCCTGTCACAGCTGTGATCCCGTGGACGCTCAGCTGATGCTGAGATT 1304
QY 115 HisProLysLysLeuProValLeuLeuGlyHisSerAlaAspLeuArgProGly 134
DB 1305 CAGACTAAGAGCCCTCCCGACGCTGCGGACGCTCAGCTGATGCTTCCGGCAGGG 1364
QY 135 GluPheValValAlaIleGlySerProPheAlaLeuGluAsnThrValThrGlyIle 154
DB 1365 GAGTTGTGTTGCCATGGGAGATCCCTTGCACAGACAGATCATCCGCGATT 1424
QY 155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspLeuArg 174
DB 1425 GTTAGCTGCTCAGCTCCAGCCAGGACCTGGAGCTCCCAACCAATGTCGAAATC 1484
QY 175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
DB 1485 ATTCAACTGATGAGCTATTGATTTGGAACTCTGAGAGTCCCTGTTAACCTGGAT 1544
QY 195 GlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIlePro 214
DB 1545 GGGAGGATGATGAGTGAACACCATGAGTCACTGAAATCTCTTGGCATCCCT 1604
QY 215 SerAspArgIleThrArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 230
DB 1605 TCTGATCTCTTCGAGACTTCTGCATCGCGGAAAGAAATCTCCTCCCGGATC 1664
QY 231 LysAspTyrLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
DB 1665 AGTGGTCCAGCGCGCTCATTTGGGTGATGATGCTGACCTGAGGCCGAGATCCTT 1724
QY 251 AspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrValGln 270
DB 1725 GCTGAACCTACAGCTTCAGAACACAGCTTCCCATGTTCAAGCATGGTACTCATCAT 1784
QY 271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
DB 1785 AAGTCATCTGGGCTCCCTCCACACCGGCTGTGCGGCTGAGTGTGATTTTG 1844
QY 291 LysValAsnGlyArgProLeuValAspSerSerGluLeuGlnGluAlaValLeuThrGlu 310
DB 1845 GCCATTGGGAGAGTGGTACAAATGCTGAAGATGTTTAAAGACGTTGGAACCAA 1904
QY 311 SerProLeuLeuGluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaPro 330
DB 1905 TCCCAATTGGCAGTGAAGATCCGCGGAGACAGAAACATGACCTTATATGTGACCTT 1964
QY 331 GluVal 332
DB 1965 GAGGTC 1970
RESULT 10
US-08-923-454A-24
Sequence 24, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karian, Eric
APPLICANT: Clinkenbeard, Helen

APPLICANT: Browne, Michael
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 603...1976
OTHER INFORMATION:
US-08-923-454A-24
Alignment Scores:
Pred. No.: 8,656-93 Length: 2187
Score: 882.00 Matches: 169
Percent Similarity: 74.8% Conservative: 72
Best Local Similarity: 52.5% Mismatches: 71
Query Match: 52.5% Indels: 10
DB: 3 Gaps: 2
US-10-617-443B-2 (1-334) x US-08-923-454A-24 (1-2187)
QY 15 SerSerProArgTyrLysPheAsnPhelLeaAAspValaIGluYerLeaLapProa 34
DB 1023 GCTTCTCCCGAGACAGACACATTTCATCCGATGCTGAGAGACACACACTGCC 1082
QY 35 ValValHsIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
DB 1083 GTGGCTCTATATGAGATCCTGACCGGCACTTTCTTGGCGCGAGGCTCCCTATCTCG 1142
QY 55 SerGlySerGlyPheIleuSerGlyLysIleuLeuLeuLeuThraAsnLysValVal 74
DB 1143 AACGGCTTCGAGTGTGGCTGCGCATGGCTCATGTGACCAACCGCCATGTGGTG 1202
QY 75 SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAsp 94
DB 1203 GCTGAT-----CGGCGCAGATGCTCGTGTGAGACTGCTAAGCGCGCAGC 1244

QY 95 SerTyrGluAlaThrIleLeuAspIleAspLysLysSerAspIleAlaThrLeuValIle 114
DB 1245 ACGTATGAGCCCGGTGTACAGCTGTGATCCCGTGAGACATGCAACGCTGAGGATT 1304
QY 115 HisProLysLysLysLeuProValLeuLeuLeuGlnHisSerAlaAspLeuArgProGly 134
DB 1305 CAGACTAAGAGACCTCTCCACGCTGCTGGAGAGCTCAGCTGATGTCGGGCAAGCG 1364
QY 135 GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrGlyIle 154
DB 1365 GAGTTGTGTTGGCATGGAGATCCCTTTCACCTGCAGAACACAGATCAATCCGCAATT 1424
QY 155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyr 174
DB 1425 GTTAGCTCTGCTCAGCGCTCCAGCAGACCTGGAGACTCCCCCAACCAATGTGGATTAC 1484
QY 175 IleGlnThrAspAlaIleLeuAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
DB 1485 ATTCAACTGATGACGATATTGATTGGAAACTCTGAGGTCCTCGTTTAACTGGAT 1544
QY 195 GlyLeuValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIlePro 214
DB 1545 GGGAGGTGATTGGAGTGAACACCATGAAGGTCAAGCTGGAAATCTCTTGGCATTCCT 1604
QY 215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln-----Ile 230
DB 1605 TCTGATGCTGCTCCAGAGATTTCTGCATGCTGGGAAAAAGAAATTCCTCTCCGGAATC 1664
QY 231 LysAspTyrLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
DB 1665 AGTGGTCCACGCGCGCTACATTGGGCTGATGATGTCGACCTCGAGTCCACGATCCTT 1724
QY 251 AspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrValGln 270
DB 1725 GCTGAACTACAGCTTCGAGAACCAAGCTTCCGATGTTCCAGCATGCTACTCATTCAT 1784
QY 271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
DB 1785 AAAGTCACTCGGGCTCCCTCCGACACCGGCTGCTGCGCGCTGGATGATTTTG 1844
QY 291 LysValAlaGlyArgProLeuValAspSerSerGluLeuGlnGluValValLeuThrGlu 310
DB 1845 GCCATTGGGAGACAGATGTCACAAATGCTGAAGTGTATTGAAGCTTTCGAAACCCA 1904
QY 311 SerProLeuLeuGluValAlaArgArgGlyAsnAspAspLeuLeuPheSerIleAlaPro 330
DB 1905 TCCAGTTGGCAGTGCAGATCCGGCGGAGACGAGAAACACTGACTTATGTGACCCCT 1964
QY 331 GluVal 332
DB 1965 GAGGTC 1970
RESULT 11
US-09-008-271A-23
Sequence 23, Application US/09008271A
Patent No. 6203979
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Vue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA

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1      ZIP: 94304
2      COMPUTER READABLE FORM:
3      MEDIUM TYPE: Diskette
4      COMPUTER: IBM Compatible
5      OPERATING SYSTEM: DOS
6      SOFTWARE: FastSeq for Windows Versi
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/09/008,271A
9      FILING DATE: 16-Jan-1998
10     PRIOR APPLICATION DATA:
11     APPLICATION NUMBER: <Unknown>
12     FILING DATE: <Unknown>
13     ATTORNEY/AGENT INFORMATION:
14     NAME: Mohan-Peterson, Sheela
15     REGISTRATION NUMBER: 41,201
16     REFERENCE/DOCKET NUMBER: PR-0458 US
17     TELECOMMUNICATION INFORMATION:
18     TELEPHONE: 650-855-0555
19     TELEFAX: 650-845-4166
20     INFORMATION FOR SEQ ID NO: 23:
21     SEQUENCE CHARACTERISTICS:
22     LENGTH: 2476 base pairs
23     TYPE: nucleic acid
24     STRANDEDNESS: single
25     TOPOLOGY: linear
26     IMMEDIATE SOURCE:
27     LIBRARY: SINITC01
28     CLONE: 2680548
29     SEQUENCE DESCRIPTION: SEQ ID NO: 23 :
30     US-09-008-271A-23

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Alignment Scores:		
Pred. No.:	1.05e-92	2476
Score:	882.00	Matches: 169
Percent Similarity:	74.8%	Conservative: 72
Score Similarity:	52.5%	Mismatches: 71
Best Local Similarity:	52.5%	Indels: 10
Query Match:	3	Gaps: 2
DB:		

US-10-617-443B-2 (1-334) X US-09-008-271A-23 (1-2476)

QY 15 SerSerProArgTgTyrLysPheAsnPhetIleIaAspValIaIaGluYrIleAlaProIa 34
 Db 481 GCTTCTCCCGGAGATGCACTACAACTTCATCGGAGATGTGTGTGAGAAAGACAGCACTCC 540
 QY 35 ValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
 Db 541 GTGTGCTATATCGAATATCCTGGACCGGCACCTTTCTTGTGGCGGAGAGTCTCTTCTCG 600
 QY 55 SerGlySerGlyPheIleMetSerGluIaGlyLeuIleIleThrAsnAlaHisValIa 74
 Db 601 AACGGCTCAGGATTCGTGTGGCTGGCCGATGGGCTCATTTGTCAACCAAGCCCATGTGGTG 660
 QY 75 SerSerAsnSerAlaIaIaProGlyArgGlnGlnLeuIaValGlnLeuGlnbndGlyAsp 94
 Db 661 GCTGAR-----CGCGCAGAGTCCGTGTGAGACTGCTAAGCGCGGAC 702
 QY 95 SerTyrGluAlaThrIleLysAspIleAspLysLysSerAspIleAlaThrIleLysIle 114
 Db 703 ACCTAATGAGCGCCGTGTACACAGCTGTGGATCCCGGTGGACAACTCCCAACGCTGAAGATT 762
 QY 115 HisProLysLysLysLeuProValIleLeuLeuGlyHisSerAlaAspLeuArgProGly 134
 Db 763 CACACATGAAGAGCGTCTCCCAACGCTGCTCTGGAGCGCTCAACTGATGTCTGGCAAGGG 822
 QY 135 GluPheValValaIaIleGlySerProPheAlaLeuGlnbndAsnThrValIThrTnGlyIle 154
 Db 823 GAGTTGTGTTCGCATGGAGAGTCCCTTTGGCACTCGAAGAACAGATCAATCCGGCAT 882
 QY 155 ValSerThrIaGlnArgGlnGlyArgGlnLeuGlyLeuArgAspSerAspMetAspTyr 174
 Db 883 GTTAAAGCTCTGTCAAGCGTCCAGCAGAGACTCTGGGACTCCCCCAACCAATGTGGAATAC 942

Oy	175	IleglnThrApAlallelleaenryrGlyaaSerSclGlyProleuValaenleuAap	194
Db	943	ATTCAAACTCATCAGCTATTGATTTTGGAAACTCGAAGTCCCTCGGTAAACCTGGAT	1002
Oy	195	GLyGLValalleGlylleaenThrleuLyValThrAglylleSerPheallePro	214
Db	1003	GGGAGAGTGATTGGAGTGAACACCATAGAGTCACAGCTGGAAATCTCTTGGCATCCCT	1062
Oy	215	SerApAlrGleThrArArgPheleuthGluPheGlnApblyeGln-----lle	230
Db	1063	TCTATAGCTCTTCAGAGTTTCGCATCGCGGGGAAAGAAGAAATCTCCTCCGGATCC	1122
Oy	231	LySaApTrpLyAlaArgPhealleGlylleArgMetArgThrIleThrProSerleuVal	250
Db	1123	AGTGGGTCCAGCGCGCGCTACATGGGGGTGATGATGTCGACCCGTAATCTCCAGATCCTT	1182
Oy	251	ApGluLeuLyAlaSerAenProApPheProGluValSerSerGlyIleTyFvalGln	270
Db	1183	GCTGAACATCAAGCTTCGAAACCAAGCTTCCCATGTTACAGATGGGTACTATCATCAT	1242
Oy	271	GluValAlaAProAenSerProSerGlnArgGlylleGlnApGlyAapAlleVal	290
Db	1243	AAAGTCATCCCGGGCTCCCTGCACACCGGGCTGGTCTGGCGCGCTGGATGTGATTTTG	1302
Oy	291	LyValaenGlyArgProleuValaApSerSerGluLeuGlnGluValaValleuThrGlu	310
Db	1303	GCCATTGGGGACCAAGATGTATCAAAATCTGAAAGATGTTTATGAAGCTGTTCGAACCCAA	1362
Oy	311	SerProleuLeuLeuGluValArgArGlyAenApApbLeuLeuPheSerlleleAPro	330
Db	1363	TCCCAATGTGGCAGTGCAGATCCGGCGGGGACGAGAAACATGACCTTATATGTGACCCCT	1422
Oy	331	GluVal	332
Db	1423	GAGGTC	1428

Qy	331	GluVal	332
Db	1423	GAGTC	1428

RESULT 12
US-09-968-415-23
Sequence 23, Application US/09968415

GENERAL INFORMATION:

1 Hillman, Jennifer L.
2 Yue, Henry
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Guégler, Naïo
Corley, Neil C.
Tang, Tom Y.

Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24

NUMBER OF PAGES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
ADDRESS: 317A Porter Dr.
CITY: San Diego, CA 92161
COUNTRY: USA
TELEPHONE: 619 594 1000
FAX: 619 594 1001
E-MAIL: info@incyte.com

SIRREI: 31/4 FO
CITY: Palo Alto
STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

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;
; OPENING SYSTEM: 20
; SOFTWARE: FastSeq for windows Version 2.0
; CURRENT APPLICATION DATA:
;                               UC/09/068 415
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APPLICATION NUMBER: 05/05/2000, 11:11
FILING DATE: 26-Sep-2001
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/659,151
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

```
; ALLIANCE/AGENCY INFORMATION  
; NAME: Mohan-Peterson, Sheela  
; REGISTRATION NUMBER: 41,201  
; REGISTRATION / COVER NUMBER: DF-0458 IIS
```

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SINVUCT01
CLONE: 2680548
SEQUENCE DESCRIPTION: SEQ ID NO: 23 :
US-09-968-415-23
Alignment Scores:
Pred. No.: 1,05e-92 Length: 2476
Score: 882.00 Matches: 169
Percent Similarity: 74.8% Conservative: 72
Best Local Similarity: 52.5% Mismatches: 71
Query Match: 52.5% Indels: 10
DB: 3 Gaps: 2
US-10-617-443B-2 (1-334) x US-09-968-415-23 (1-2476)
QY 15 SerSerProArgTyllysPheAsnPhelIeAlaAspValaGlulysIleAlaProAla 34
DB 481 GCTTCTCCCGAGTCAAGTCACTTCATCGAGATGTGTGAGAGACAGACACTGCC 540
QY 35 ValValHsIleGlulysPheLeuArgHsIleProLeuPheGlYArgAsnValProLeuSer 54
DB 541 GTGGCTATATGAGATCCTGGACCGGACCTTTCTTGGGCGGAGGCTCCTATCTCG 600
QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyIleIleThrAsnAlaHisValVal 74
DB 601 AACGGCTAGATTCGTGGTGGCTCCGATGCGCTCATTTGTCACCAACGCCCATGTGTG 660
QY 75 SerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGlnLeuGlnAsnGlyAsp 94
DB 661 GCTGAT-----CGGCCAGAGTCCGTGTAGACTGCTAAGCGGCGAC 702
QY 95 SerTyrGluAlaThrIleLysAspIleAspLysSerAspIleAlaThrIleLysIle 114
DB 703 ACGTATGAGCGCGGTGTCACAGCTGTGATCCCGGCGAGACATCGCAACGCTGAGGATT 762
QY 115 HisProLysLysLysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGly 134
DB 763 CAGACTAAGAGACCTCTCCCAACGCTGCTGGAGCGCTCAAGTGTCTCGGCAAGGG 822
QY 135 GluPheValaIleAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
DB 823 GAGTTTGTGTTCCTGCAATGGAGATCCCTTTGCACTGCAAGACATCATCCGGCATTT 882
QY 155 ValSerThrAlaGlnArgGlnGluLysArgGluLeuArgAspSerAspMetAspTyr 174
DB 883 GTTACTCTGCTCAGCGTCCAGCGCAGAGACTGGGACTCCCAACCAAGATGGAAATAC 942
QY 175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValAsnLeuAsp 194
DB 943 ATTCAACTGATGAGCTATTGATTTTGGAACTGTGAGAGGCTCCCTGGTTAACTGGAT 1002
QY 195 GlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIlePro 214
DB 1003 GGGAGGTGATTTGAGTGAACCATGAAAGGTCAAGCTGGAAATCTCTTGCCATTCCT 1062
QY 215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln-----Ile 230
DB 1063 TCTGATCGTCTTCGAGAGTTTCTGCATCGCTGGGAAAGAAAGAAATTCCTCCGGGAATC 1122
QY 231 LysAspTlpyLysLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
DB 1123 AGTGGTCCCAAGCGCGCTACATTTGGGGGATGATGATGATCCCTGAGTCCCGCATCTCT 1182
QY 251 AspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyrValGln 270

DB 1183 GCTGAACACAGCTTCGAGAGACCAAGCTTTCCCATGTTTCAGCATGTGTACTATCCAT 1242
QY 271 GluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIleVal 290
DB 1243 AAAGTCATCTGGGCTCCCTGCAACACCGGGCTGTGCGGCTCTGATGTGATTTTG 1302
QY 291 LysValaGlnGlyArgProLeuValAspSerSerGluLeuGlnGluValaValLeuThrGlu 310
DB 1303 GCCATTGGGAGACGATGTATCAAAATGCTGAAGATTTTAAAGCTGTTCGAACCCAA 1362
QY 311 SerProLeuLeuGluValaLysArgGlyLysAsnAspLeuLeuPheSerIleAlaPro 330
DB 1363 TCCAGTTGGCAGCTGCATATCCGGCGGAGAGAAACATGACTTATATGTACACCTT 1422
QY 331 GluVal 332
DB 1423 GAGGTC 1428
RESULT 13
US-08-923-454A-30
Sequence 30, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karren, Eric
APPLICANT: Clinkdeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southan, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS: 40
ADDRESSER: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pasteo Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923, 454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEPT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33, 833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE: Polymorphic variants at 672 and 1435
FEATURE: aa24=Arg/Cys aa278=Ala/Val
NAME/KEY: Coding Sequence

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LOCATION: 603...1976
OTHER INFORMATION:
US-08-923-454A-30

Alignment Scores:
Pred. No.: 2,54e-92      Length: 2187
Score: 878.00           Matches: 168
Percent Similarity: 74.5%  Conservative: 72
Best Local Similarity: 52.2%  Mismatches: 72
Query Match: 52.3%      Indels: 10
DB: 3                    Gaps: 2

US-10-617-443B-2 (1-334) x US-08-923-454A-30 (1-2187)

QY 15 SerSerProArgTyrIlePheAsnPhenIleAlaAspValaIglulysIleAlaProAla 34
DB 1023 GCTTCTCCCGGAGTACAGTACATTCTGCGAGATGCTGTGAGAGAACACACACTGCGC 1082
QY 35 ValValaIleIleIglulPheLeuArgHISProLeuPheGlyArgAsnValaProLeuSer 54
DB 1083 GTGCTATATATGAGATCTGAGCCGCGACCTTCTTGGCGCGCGAGGTCTCTATCTG 1142
QY 55 SerGlySerGlyPheIleMetSerGlyAlaGlyLeuIleIleThrAsnAlaHisVala 74
DB 1143 AACGGCTCAGGATTCGTGGTGGCTGCGATGGGCTCATGTGTACCAACGCCCATGTGTG 1202
QY 75 SerSerAsnSerAlaAlaProGlyArgGlnIleuLysValaGlnLeuGlnAsnGlyAsp 94
DB 1203 GCTGAT-----CGGCGCAGAGTCGCTGTGAGACTGCAAGCGCGAGC 1244
QY 95 SerTyrGluAlaThrIleLysAspIleAspLysSerAspIleAlaThrIleLysIle 114
DB 1245 ACCTATGAGGCCCTGTGGCAGCTGCGATCCGTGGCAACAATCGAACGCTGAGGATT 1304
QY 115 HisProLysLysLysLeuProValIleuLysGlyHisSerAlaAspLeuArgProGly 134
DB 1305 CAGACTRAGAGGCTCTCCCGACGCTGCTCTGGGACGCTGAGTGTCCGCAAGGG 1364
QY 135 GluPheValaValaIleGlySerProPheAlaLeuGlnAsnThrValaThrThrGlyIle 154
DB 1365 GAGTTGTGTGTCATGAGGAGAGTCCCTTGCACCTGCAGAACAGACATCGGCAAT 1424
QY 155 ValSerThrAlaGlnArgGluGlyArgGlnLeuGlyLeuArgAspSerAspMetAspTyr 174
DB 1425 GTTAGCTCTCTCGGCTCCAGCCAGACCTGGGACTCCCGCAACCAATGTGGAAATC 1484
QY 175 IleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValaAsnLeuAsp 194
DB 1485 ATTCAAACTGATGACGATATTGATTGGAACCTGAGAGTCCCTGTGTAACCTGGAT 1544
QY 195 GlyGluValaIleGlyIleAsnThrLeuLysValaThrAlaGlyIleSerPheAlaIlePro 214
DB 1545 GGGAGGTGATGAGGAGAACACATGAAAGTCACTGAGTGAATCTCTTGTCCATCTCT 1604
QY 215 SerAspArgIleThrArgPheLeuThrGlnPheGlnAspLysGln-----Ile 230
DB 1605 TCTATGCTCTTCGAGACTTCTCTGATCGTGGGAAAAAGAAAGATTCTCTCCCGAATC 1664
QY 231 LysAspTyrLysLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
DB 1665 AGTGGGTCCAGCGCGCTGATGAGTGGGTGATGAGTCCGAGTCCGAGCATCTCT 1724
QY 251 AspGluLeuLysValaSerAsnProAspPheProGluValaSerSerGlyIleTyrValGln 270
DB 1725 GCTGAACACAGCTTCGAGAACCAAGCTTCCCATGTTCAGCATGTGTATCTCATCAT 1784
QY 271 GluValaIleProAsnSerProSerGlnArgGlyIleGlnAsnGlyAspIleIleVal 290
DB 1785 AAAGTCATCCCGGCTCCCTGCAACACCGGCTGGTCTGCGGCGCTGATGTATTTTG 1844
QY 291 LysValaIleGlyArgProLeuValaAspSerSerGluLeuGlnGluValaValLeuThrGlu 310
DB 1845 GCCATTGGGAGCAGATGATGTAACAAATCTGAAGATGTTATGAAGCTGTTGCAACCCA 1904

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QY 311 SerProLeuLeuGlnValaArgArgGlyAsnAspAspLeuPheSerIleAlaPro 330
DB 1905 TCCAGTTGGCAGATCGATCCGCGGAGAGAAACACTGACCTTATATGTGACCTT 1964
QY 331 GluVala 332
DB 1965 GAGGTC 1970

RESULT 14
US-08-923-454A-3
Sequence 3, Application US/08923454A
Patent No. 6004794
GENERAL INFORMATION:
APPLICANT: Creasy, Caretha
APPLICANT: Livi, George
APPLICANT: Karren, Eric
APPLICANT: Clinkenbeard, Helen
APPLICANT: Browne, Michael
APPLICANT: Southern, Christopher
TITLE OF INVENTION: HUMAN SERINE PROTEASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Smithline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Pasteo Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/923,454A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/025436
FILING DATE: 06-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50547
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1787 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-923-454A-3

Alignment Scores:
Pred. No.: 2,27e-87      Length: 1787
Score: 834.50           Matches: 169
Percent Similarity: 60.7%  Conservative: 72
Best Local Similarity: 42.6%  Mismatches: 71
Query Match: 49.7%      Indels: 85
DB: 3                    Gaps: 3

US-10-617-443B-2 (1-334) x US-08-923-454A-3 (1-1787)

QY 15 SerSerProArgTyrIlePheAsnPhenIleAlaAspValaIglulysIleAlaProAla 34

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Db      259 GCTTCTCCCGGAGTCAGTCACTTCAGTGTGGAGAAAGACGACCTGCC 318
Qy      35 ValValaHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
Db      319 GTGGCTTATTCGAGATCTTGGACCGGACCTTCTTGGGGCCGAGAGTCCCTATCTCG 378
Qy      55 SerGlySerGlyPheIleMetSerGluIleGlyLeuIleIleThrAsnAlaHisValVal 74
Db      379 AACGGCTCAGATTCGTGTGCTCCAGATGGCTCATTTGTCACCAAGCCCATGTGGTG 438
Qy      75 SerSerAsnSerAlaAlaProGlyArgGlnLeuLeuValGlnLeuGlnAsnGlyAsp 94
Db      439 GCTGAT-----CGGGCAGAGTCCGTGTGAGACTGTAAAGCGGCAC 480
Qy      95 SerTyrgluAlaThrIleLeuAspIleAspIleAspIleAspIleAlaThrIleAspIle 114
Db      481 ACGTATGAGCGCGTGTGACAGCTGTGATCCCGTGGCAGACATCGCAACGCTGGAGATT 540
Qy      115 HisProLysLysLysLeuProValLeuLeuLeuGlnHisSerAlaAspLeuAspProGly 134
Db      541 CAGACTAAGAGCCCTCTCCACGCTGCTGGACGCTGAGATGTCGGGCAAGG 600
Qy      135 GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
Db      601 GAGTTTGTGTGGCATGGGAAGTCCCTTTCACCTGACGAGAACACATCATCCGGCATT 660
Qy      155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlnLeuArgAspSerAspMetAspTyr 174
Db      661 GTTAGCTCTGCTCAGCGCTCAGCCAGACAGCTGGGACCTCCCAACCAATGTGAATAC 720
Qy      175 IleGlnThrAspAlaIleIleAsnTyrGlyLysAsnSerGlyProLeuValAsnLeu--- 193
Db      721 ATTCAACTGATGACGCTATTGATTTGAAACTGAGAGGCCCTGCTTAACCTGGTG 780
Qy      193 ----- 193
Db      781 AGTAGACATCTTCCTTCCAAGATCCCTGCGCCAGGTCAGTGTGGGAAGGTAGTTT 840
Qy      193 ----- 193
Db      841 CCCCTAATTCAGAGATGTTGGTCAAGTTCGACAGTTCCTTGTGGCTATCTCTCA 900
Qy      193 ----- 193
Db      901 TATCCAACCAATCTCCCAACACTTCTGCTGACTTTTGTGGGTGCCCATCCCTA 960
Qy      194 ----- 194
Db      961 CTATTTGTTAGGCTAGGGAATGGGGGCTGTATCCCTGACAGATGGGGAGGTGATTGA 1020
Qy      200 IleAsnThrLeuLysValIleThrAlaGlyIleSerPheAlaIleProSerAspArgIleThr 219
Db      1021 GTGAACACCAATGAAAGTCAACAGCTGGAATCTCTTGCATCCCTTGCATGCTGTGCA 1080
Qy      220 ArgPheLeuThrGlnPheGlnAspLysGln-----IleLysAspTyrLysLys 235
Db      1081 GAGTTTCTGCATCGTGGGGAAGAAAGAAATTCCTCCCGAATCAAGTGGTCCGAGGG 1140
Qy      236 ArgPheIleGlyIleArgMetArgThrIleThrProSerLeuValAspGluLeuValAla 255
Db      1141 CGCTACATTTGGGGTATGATCTGACCTGATCCCAACATCCTTGCMACTACAGCTT 1200
Qy      256 SerAsnProAspPheProGluValSerSerGlyIleTyrValGlnGlnValAlaProAsn 275
Db      1201 CGAGAACCAACCTTTCCGATGTTTCAGCATGTGTGACTCATCAATAAGTCACTCTGGGC 1260
Qy      276 SerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArg 295
Db      1261 TCCCTTGACACCGGGCTGTGCTGGCTGTGATGATTTTGGCCATTGGGAGAGAG 1320
Qy      296 ProLeuValAspSerSerGlnLeuGlnGlnValAlaValLeuThrGlnSerProLeuLeu 315

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RESULT 15
US-08-923-454A-26
; Sequence 26, Application US/08923454A
; Patent No. 6004794
; GENERAL INFORMATION:
; APPLICANT: Creasy, Caretha
; APPLICANT: Livi, George
; APPLICANT: Karen, Eric
; APPLICANT: Climbendard, Helen
; APPLICANT: Browne, Michael
; APPLICANT: Southan, Christopher
; TITLE OF INVENTION: HUMAN SERINE PROTEASE
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESS: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTA/Seq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,454A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/025436
; FILING DATE: 06-SEPT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P50547
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2551 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: NO
; ORIGINAL SOURCE:
; FEATURES:
; NAME/KEY: Coding Sequence
; LOCATION: 603..1733
; OTHER INFORMATION:
US-08-923-454A-26

Alignment Scores:
Pred. No.: 3,93e-87 Length: 2551
Score: 834.50 Matches: 169
Percent Similarity: 60.7% Conservative: 72
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US-10-617-443B-2 (1-334) x US-08-923-454A-26 (1-2551)

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QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValVal 74
Db 1143 AACGGCTCAGATTCCTGGTGGCTGCATGATGTCACCAACGCCCATGTGGTG 1202
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Db 1305 CAGACTAAGAGCGCTCTCCCGACGCTGCGCTGAGAGCTCACTATGTCGGCAGAGG 1364
QY 135 GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
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QY 220 ArgPheLeuThrGluPheGlnAspIleGln-----IleAspTrpIleAsp 235
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Db 1965 CGAGAACCAAGCTTTCGCGATGTTTCAGCATGTGTACTCTCCATTAAGTCACTCGG 2024
QY 276 SerProSerGlnArgGlyIleGlnAspGlyAspIleIleValIleValAsnGlyArg 295
Db 2025 TCCCTGTGACACCGGGGCTGTCTGCGGCTGTGATGTGATTTGGCCATTTGGGGAGCAG 2084
QY 296 ProLeuValAspSerSerGluLeuGlnGluAlaValLeuThrIleSerProLeuLeu 315
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QY 316 GluValArgArgGlyAsnAspAspLeuLeuPheSerIleAlaProGluVal 332
Db 2145 CAGATCCGGCGGGGACGAGAAACACTGACTTATATGTGACCCCTGAGGTT 2195
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Job time : 231 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 21, 2006, 20:37:21 : Search time 823 Seconds

(without alignments)
3355.981 Million cell updates/sec

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NOR=ext
-HEADSIE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs803p
-USER=US10617443 @CGN 1.1 1549 @runat.21022006.165828.17349 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications.NA.Main:

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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1679	100.0	3006	6	US-10-617-443B-1
3	1635	97.4	1044	3	US-09-796-858-9
4	1635	97.4	1563	3	US-09-796-753-33
5	1635	97.4	1797	7	US-10-275-505-28
6	1635	97.4	1797	10	US-11-140-224-28
7	1635	97.4	2040	3	US-09-818-143-14

8	1635	97.4	2094	7	US-10-381-820A-7	Sequence 7, Appli
9	1635	97.4	2541	9	US-10-956-157-5181	Sequence 5181, Ap
10	1635	97.4	2543	9	US-10-485-313A-31	Sequence 31, Appl
11	1635	97.4	2576	3	US-09-796-753-31	Sequence 31, Appl
12	1536	91.5	2450	9	US-10-485-313A-26	Sequence 26, Appl
13	1482.5	88.3	2551	6	US-10-301-822-78	Sequence 78, Appl
14	1378	82.1	1868	3	US-09-764-898-112	Sequence 112, App
15	1122	66.8	1695	3	US-09-969-384-7	Sequence 7, Appli
16	1117	66.5	1953	9	US-10-485-313A-32	Sequence 32, Appl
17	1105	65.8	1788	3	US-09-764-898-40	Sequence 40, Appl
18	1057	63.0	1897	9	US-10-485-313A-38	Sequence 38, Appl
19	1034.5	61.6	1440	3	US-09-796-858-7	Sequence 7, Appli
20	1034.5	61.6	1894	6	US-10-104-047-795	Sequence 795, App
21	1034.5	61.6	2034	3	US-10-102-524-1332	Sequence 132, Ap
22	1034.5	61.6	2036	3	US-09-960-706-516	Sequence 516, App
23	1034.5	61.6	2036	6	US-10-170-385-356	Sequence 356, App
24	1034.5	61.6	2036	6	US-10-17-118-815	Sequence 815, App
25	1034.5	61.6	2036	6	US-10-342-887-815	Sequence 815, App
26	1034.5	61.6	2036	8	US-10-772-636-47	Sequence 47, Appl
27	1034.5	61.6	2036	9	US-10-956-157-919	Sequence 919, App
28	1034.5	61.6	2054	5	US-10-084-817-32	Sequence 32, Appl
29	1034.5	61.6	2437	5	US-10-196-846-10826	Sequence 10826, A
30	1027.5	61.2	2157	6	US-10-264-049-135	Sequence 135, App
31	1006.5	59.9	1855	3	US-09-925-298-134	Sequence 134, App
32	1006.5	59.9	1855	5	US-10-102-806-134	Sequence 134, App
33	1005.5	59.9	2212	8	US-10-723-860-5299	Sequence 5299, Ap
34	981.5	58.5	1534	3	US-09-765-231A-20	Sequence 20, Appl
35	945	56.3	1328	9	US-10-764-420-1506	Sequence 1506, Ap
36	920	54.8	1859	3	US-09-866-050A-588	Sequence 588, App
37	920	54.8	1859	5	US-10-152-661-588	Sequence 588, App
38	890	53.0	1544	8	US-10-789-241-49	Sequence 49, Appl
39	890	53.0	1544	8	US-10-772-636-7	Sequence 7, Appli
40	890	53.0	1553	3	US-09-935-390A-18	Sequence 18, Appl
41	882	52.5	963	7	US-10-730-476A-11	Sequence 11, Appl
42	882	52.5	963	9	US-10-730-476A-11	Sequence 11, Appl
43	882	52.5	975	7	US-10-730-476A-1	Sequence 1, Appli
44	882	52.5	975	9	US-10-730-476A-1	Sequence 1, Appli
45	882	52.5	1374	5	US-10-197-634-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-189-099A-1
; Sequence 1, Application US/10189099A
; Publication No. US20040005659A1
; GENERAL INFORMATION:
; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jjian-shen
; APPLICANT: Chen, Callin
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/189, 099A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: CDNA
; ORGANISM: Homo sapiens
US-10-189-099A-1

Alignment Scores:

Pred. No.: 3,93e-180
Score: 1679.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 6
Gaps: 0
US-10-617-443B-2 (1-334) x US-10-189-099A-1 (1-3006)

Length: 3006
Matches: 334
Conservative: 0
Mismatch: 0
Indels: 0

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      1071 TTCACATTCATTCCTGACGCTGCGAGAGATCGCACACCCCTGGCTCCATAGAGCTC 1130
Qy      41 PheleuArgHisProleuPheGlyArgAsnValProleuSerSerGlySerGlyPheIle 60
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Qy      61 MetSerGluAlaGlyLeuIleIleThrAsnAlaHisiValIaIaSerSerAsnSerAlaIa 80
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Qy      121 ProValleuLeuLeuGlnHisSerAlaAspLeuArgProGlyGluPheValValAlaIaIle 140
      1371 CCGTGTGTGTGCTGGGTCACTCGGCCGACCTCGGCTGGGAGTTGTGTGGGCTCATC 1430
Qy      141 GlySerProPheAlaIaIaGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArg 160
      1431 GGCAGTCCCTTCCGCTCAGAACACAGTACACGAGCAACGGGCTCTGACAGCTGCCAGCG 1490
Qy      161 GluGlyArgGluGlnleuYsValArgAspSerAspMetAspTyrIleGlnThrAspAlaIle 180
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RESULT 2
US-10-617-443B-1

; Sequence 1, Application US/10617443B
; Publication No. US2005001977A1
; GENERAL INFORMATION:

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; APPLICANT: Darrow, Andrew L
; APPLICANT: Qi, Jian-shen
; APPLICANT: Chen, Caifan
; APPLICANT: Andrade-Gordon, Patricia
; TITLE OF INVENTION: Human PRSS-11 like S2 serine protease and uses thereof
; FILE REFERENCE: ORT-1644
; CURRENT APPLICATION NUMBER: US/10/617,443B
; CURRENT FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3006
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-617-443B-1

Alignment Scores:
Pred. No.: 3,93e-180 Length: 3006
Score: 1679.00 Matches: 334
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-617-443B-2 (1-334) x US-10-617-443B-1 (1-3006)

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Qy      121 ProValleuLeuLeuGlnHisSerAlaAspLeuArgProGlyGluPheValValAlaIaIle 140
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Qy      141 GlySerProPheAlaIaIaGlnAsnThrValThrThrGlyIleValSerThrAlaGlnArg 160
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      1491 GAGGGCAGGAGCTGGGCTCCGAGACTCCGACATGACATCAAGGTCAAGGTCAAGGTCAAG 1550
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 QY 321 AsnAspAspLeuLeuPheSerIleAlaProGluValaMet 334
 Db 1971 AACGACGACTCTCTCTTCAAGCATCCGACCTGAGGTGTCATG 2012

RESULT 3

US-09-796-858-9
 ; Sequence 9, Application US/09796858
 ; Patent No. US20020055139A1

GENERAL INFORMATION:

; APPLICANT: Holtezman, Douglas
 ; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC,
 ; FILE REFERENCE: PREVENTIVE, THERAPEUTIC, AND OTHER USES
 ; FILE REFERENCE: 7853-226-999
 ; CURRENT APPLICATION NUMBER: US/09/796, 858
 ; PRIOR APPLICATION NUMBER: 09/223, 094
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/223, 546
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/224, 246
 ; PRIOR FILING DATE: 1998-12-30
 ; PRIOR APPLICATION NUMBER: 09/312, 359
 ; PRIOR FILING DATE: 1999-05-14
 ; PRIOR APPLICATION NUMBER: 09/336, 536
 ; PRIOR FILING DATE: 1999-06-18
 ; PRIOR APPLICATION NUMBER: 09/342, 687
 ; PRIOR FILING DATE: 1999-06-29
 ; PRIOR APPLICATION NUMBER: 09/399, 723
 ; PRIOR FILING DATE: 1999-09-20
 ; PRIOR APPLICATION NUMBER: 09/471, 179
 ; PRIOR FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: 09/474, 071
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/474, 072
 ; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: 09/572, 002
 ; PRIOR FILING DATE: 2000-05-14
 ; PRIOR APPLICATION NUMBER: 09/597, 993
 ; PRIOR FILING DATE: 2000-06-12
 ; PRIOR APPLICATION NUMBER: 09/599, 596
 ; PRIOR FILING DATE: 2000-06-22
 ; PRIOR APPLICATION NUMBER: 09/606, 565
 ; PRIOR FILING DATE: 2000-06-29
 ; PRIOR APPLICATION NUMBER: 09/365, 164
 ; PRIOR FILING DATE: 1999-07-30
 ; PRIOR APPLICATION NUMBER: 09/630, 334
 ; PRIOR FILING DATE: 2000-07-31
 ; PRIOR APPLICATION NUMBER: 09/665, 666
 ; PRIOR FILING DATE: 2000-09-20
 ; NUMBER OF SEQ ID NOS: 50
 ; SEQ ID NO 9
 ; LENGTH: 1044
 ; TYPE: DNA
 ; ORGANISM: Mouse
 US-09-796-858-9

Alignment Scores:

Pred. No.: 8-756-176 Length: 1044
 Score: 1635.00 Matches: 325
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 3 Gaps: 0

US-10-617-443B-2 (1-334) x US-09-796-858-9 (1-1044)

QY 10 GlyLeuHileGlnLeuSerSerProArgTyrIlyPheAsnPhelIleAlaAspValaGlu 29
 Db 70 GGTCTCCACAGCTGAGCAGCCCGCTAAGATTCACTTCACTTGACGTGGAG 129
 QY 30 LysIleAlaProAlaValaIleIleGluLeuPheLeuArgHisProLeuPheIlyArg 49
 Db 130 AAGATCGACCAAGCGGTGTGCACATAGAGCTTCTTCGAGACACCCGCTGTTGGCGG 189
 QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
 Db 190 AACGTGCCCTCTGTCAGCGGTTCTGGCTTCATCATGTCAAGAGCCGCTGATCATCAC 249
 QY 70 AsnAlaHisValaIleSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValaGln 89
 Db 250 AATGCCCAAGTGTGTCCAGCAACAGTCTGCCCGGCAAGCACTCAAGGTGCAG 309
 QY 90 LeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIleAspIlySerAspIle 109
 Db 310 CTACAGAAATGGGGACTCTTAAGAGGCCCAATCAAGACATCGACAMAGTCGACACTT 369
 QY 110 AlaThrIleLysIleHisProLysLysAspProValaLeuLeuGlyHisSerAla 129
 Db 370 GCCACCATAGATCATCTCCAGAAAGCTCTGTTGTTGTTCTGGGTCACTCGGCC 429
 QY 130 AspLeuArgProGlyGluPheValaValaIleGlySerProPheAlaLeuGlnAsnThr 149
 Db 430 GACCTGGCGGCTGGGGAATTTGTGGTGCATCGGCACTTCCTTCCCTACAGAACCA 489
 QY 150 ValThrThrGlyIleValaSerThrAlaGlnArgGluGlyArgGluLeuArgAsp 169
 Db 490 GTGACMAAGGCACTGTCAGACATGCCCCAGGGGAGGAGGAGGAGTGGCTCCGGGAGC 549
 QY 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro 189
 Db 550 TCCGACATGAGCTGATCATCAAGCGATCCATCATCACTCGGAACTCCGGGGAGCA 609
 QY 190 LeuValaLeuLeuAspGlyGluValaIleGlyIleAsnThrLeuLysValaThrAlaGlyIle 209
 Db 610 CTGGTGAACCTGGAATGGGAGGTCAATTGGCATCAACAGCTCAAGTCCAGGCTGGCATC 669
 QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspIlyGln 229
 Db 670 TCTTTGGCATCCCTCCAGCCGATCAACAGGTTCTCCACAGAGTTCCAGAGCAAGCAG 729
 QY 230 IleLysAspTyrPlyLysArgPheIleGlyIleArgMetArgTyrIleThProSerLeu 249
 Db 730 ATCAAGAGCTGAGAGAGCGCTTCACTCGCATACGAGATGCGGACATACACCAAGCTTG 789
 QY 250 ValaAspGluLeuValaSerAsnProAspPheProGluValaSerSerGlyIleTyVala 269
 Db 790 GTGATGAGCTGAGAGGCGCAGCAACCCGCACTTCCAGAGGTGACAGGAATTTATGTG 849
 QY 270 GlnGluValaIleProAsnSerProSerGlnArgIlyIleGlnAspGlyAspIleIle 289
 Db 850 CAAGAGTGTGGCCGAATTCACCTTCTCAGAGAGCGGCATCCAGAGTGTGACATCTATC 909
 QY 290 VallyValaAsnGlyArgProLeuValaAspSerSerGluLeuGlnGluAlaValleuThr 309
 Db 910 GTCAAGATCAAGGCGCTCTTCTAGTGAATCGAGTGAAGCTGCAAGAGCCGCTGTCAC 969
 QY 310 GluSerProLeuLeuLeuGluValaArgArgIlyAsnAspAspLeuLeuPheSerIleAla 329
 Db 970 GAGTCTCTCTCTAATGAGGTGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1029

OY 330 ProgluValValMet 334
 |||||
 Db 1030 CCTGAGGTGTCATG 1044

RESULT 4

US-09-796-753-33
 Sequence 33, Application US/09796753
 Publication No. US20030027998A1
 GENERAL INFORMATION:

APPLICANT: McCarthy, Sean A.
 TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 FILE REFERENCE: 7853-227-999
 CURRENT APPLICATION NUMBER: US/09/796,753
 CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 09/183,175
 PRIOR FILING DATE: 1998-10-30
 PRIOR APPLICATION NUMBER: 09/223,094
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/223,546
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/224,246
 PRIOR FILING DATE: 1998-12-30
 PRIOR APPLICATION NUMBER: 09/259,388
 PRIOR FILING DATE: 1999-02-26
 PRIOR APPLICATION NUMBER: 60/122,458
 PRIOR FILING DATE: 1999-03-01
 PRIOR APPLICATION NUMBER: 09/312,359
 PRIOR FILING DATE: 1999-05-14
 PRIOR APPLICATION NUMBER: 09/336,536
 PRIOR FILING DATE: 1999-06-18
 PRIOR APPLICATION NUMBER: 09/342,687
 PRIOR FILING DATE: 1999-06-29
 PRIOR APPLICATION NUMBER: 09/345,464
 PRIOR FILING DATE: 1999-06-30
 PRIOR APPLICATION NUMBER: 09/365,164
 PRIOR FILING DATE: 1999-07-30
 PRIOR APPLICATION NUMBER: 09/399,723
 PRIOR FILING DATE: 1999-09-20
 PRIOR APPLICATION NUMBER: 09/409,634
 PRIOR FILING DATE: 1999-09-30
 PRIOR APPLICATION NUMBER: 09/471,179
 PRIOR FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 09/474,071
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/474,072
 PRIOR FILING DATE: 1999-12-29
 PRIOR APPLICATION NUMBER: 09/514,010
 PRIOR FILING DATE: 2000-02-25
 PRIOR APPLICATION NUMBER: 09/516,745
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: 09/572,002
 PRIOR FILING DATE: 2000-05-14
 PRIOR APPLICATION NUMBER: 09/597,993
 PRIOR FILING DATE: 2000-06-19
 PRIOR APPLICATION NUMBER: 09/599,596
 PRIOR FILING DATE: 2000-06-22
 PRIOR APPLICATION NUMBER: 09/630,334
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: 09/606,565
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 09/606,317
 PRIOR FILING DATE: 2000-06-29
 PRIOR APPLICATION NUMBER: 09/665,666
 PRIOR FILING DATE: 2000-09-20
 PRIOR APPLICATION NUMBER: 09/677,751
 PRIOR FILING DATE: 2000-09-30
 NUMBER OF SEQ ID NOS: 162
 SEQ ID NO 33
 LENGTH: 1563
 TYPE: DNA
 ORGANISM: Mouse
 US-09-796-753-33

Alignment Scores:

Pred. No.: 1,576-175
 Score: 1635.00
 Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 97.4%
 DB: 3
 Gaps: 0

US-10-617-443b-2 (1-334) x US-09-796-753-33 (1-1563)

OY 10 GIyleuHIGlnLeuSerSerProArgTyrIysPheanPheIleAlaAspValValGlu 29
 |||||
 Db 337 GGTCTCCACAGCTGAGCGCCGCGCTACAAAGTTCAACTTCATGCTGAGCTGTGAG 396
 OY 30 LysIleAlaProAlaValAlaHisIleGluPheLeuAlaGHisPProLeuPheGlyArg 49
 |||||
 Db 397 AAGATCGACACCGCTGTGTCACATAGAGCTCTTCGAGACACCCGCTGTTGGCCGC 456
 OY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
 |||||
 Db 457 AACGTGCCCTGTCAGAGGTTCTGGCTTCATCATGTGAGAGCCGCTGATCATACCC 516
 OY 70 AsnAlaHisValValSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuValGln 89
 |||||
 Db 517 AATGCCACAGTGTGTCCAGCAACAGTGTGCCCCGCGACGACAGCTCAAGGTGACG 576
 OY 90 LeuGlnaNGlyAspSerTyrGluAlaThrIleLysAspIleAspLysSerAspIle 109
 |||||
 Db 577 CTACAGAAATGGGACTCTTATGAGGCCACATCAAGACATCGACMAAGTCCGACATT 636
 OY 110 AlaThrIleLysIleHisProLysLysLysLeuProValIleLeuLeuGlyHisSerAla 129
 |||||
 Db 637 GCCACCATCAAGATCATCATCCAAAGAAAGCTCCCTGTGTGTGTGTGTGTGTGTGTGT 696
 OY 130 AspLeuArgProGlyGluPheValAlaIleIleGlySerProPheAlaLeuGlnaThr 149
 |||||
 Db 697 GACCTGCCGCTGGGAGATTGTGGTGCCATCGGACATCCCTTCGCTACAGAACACA 756
 OY 150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuArgAsp 169
 |||||
 Db 757 GTGACAAAGGCGATGTGAGCATGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 816
 OY 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyPro 189
 |||||
 Db 817 TCCGACATGAGCATCATCATCAGATGCCATCATCATCAGGAACTCCGGGGAGACA 876
 OY 190 LeuValaAsnLeuAspGlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIle 209
 |||||
 Db 877 CTGGTGAACCTGAGATGGCGAGGTGATGGCATCAACGCTCAAGGTCACGGCTGGCATC 936
 OY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnaAspLysGln 229
 |||||
 Db 937 TCCITTGCCATCCCTCAGACCGATCAGACAGGTTCTCCAGAGAGTTCCAAAGACAGAG 996
 OY 230 IleLysAspTyrLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
 |||||
 Db 997 ATCAAAAGACTGGAAGAGCGCTTCATGGCATAGAGATGGGAGATCACCAAGGCTG 1056
 OY 250 ValAspGluLeuLysValaSerAsnProAspPheProGluValaSerSerGlyIleTyrVal 269
 |||||
 Db 1057 GTGGATGAGCTGAAGGCGACAGCAACCCGAGCTCCAGAGGTCACAGAGTAATTATGTG 1116
 OY 270 GlnGluValAlaProAsnSerProSerGlnaArgIleGlyIleGlnaAspGlyAspIle 289
 |||||
 Db 1117 CAAAGGTTGCGCGAATTCCTTCAGAGAGCGGACATCAAGAGTGGAGACATATTC 1176
 OY 290 ValLysValaNGlyArgProLeuValaAspSerSerGluLeuGlnGlnAlaValaLeuThr 309
 |||||
 Db 1177 GTCAAGGTCAAGGCGGCTCTCTAGTGAATCTGAGTGAAGTGAAGGAGGCGCTGTGACC 1236
 OY 310 GluSerProLeuLeuLeuGluValaArgArgGlyAsnAspAspLeuLeuPheSerIleAla 329
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FILE REFERENCE: PI-0085 USN
CURRENT APPLICATION NUMBER: US/11/140,224
PRIOR FILING DATE: 2005-05-31
PRIOR APPLICATION NUMBER: US/10/275,505
PRIOR FILING DATE: 2002-11-04
PRIOR APPLICATION NUMBER: PCT/US01/14651
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/209,402
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 60/207,477
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/205,803
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: 60/203,566
PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: 60/202,082
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 28
LENGTH: 1797
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7474343CB1
US-11-140-224-28
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Alignment Scores:
Pred. No.: 1,92e-175 Length: 1797
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 10 Gaps: 0
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US-10-617-443B-2 (1-334) x US-11-140-224-28 (1-1797)

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QY 10 GlyLeuHISGlnLeuSerSerProArgTyrLysPheAsnPhelLeaAspValValGlu 29
DB 565 GGTCTCCACCAAGCTGAGCAGCCCGCTCAAGTTCACTTCTGTCAGCGTGGAG 624
QY 30 LysIleAlaProAlaValAlaHisIleGluLeuPheLeuArgHisProLeuPheGlyArg 49
DB 625 AAGATCGACACGCGGTGTCACATAGAGCTCTTCTGAGACACCGCGTTGCGCCG 684
QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
DB 685 AACGTGCCCCCTGTCCAGCGGTCTGCTCATCATGTCAGAGGCCGCGCTGATCATCACC 744
QY 70 AsnAlaHisIleValAlaSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuLysValGln 89
DB 745 AATGCCCACTGCTGTCTCCAGCAAGTCTGCCCCCGGCGAGGAGGAGCTCAAGGTGCGAG 804
QY 90 LeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIleAspLysLysSerAspIle 109
DB 805 CTACAGAAATGGGAGCTCTATGAGGCCACCATCAAGACATCGACAAGAGTCCGACATT 864
QY 110 AlaThrIleLysIleHisProLysLysLysLeuProValLeuLeuLeuGlyHisSerAla 129
DB 865 GCCACCATCAAGATCCATCCCAAGAAAGCTCCGTGTGTGTGCTGGGTCACTCGGCC 924
QY 130 AspLeuArgProGlyLysPheValValAlaIleGlySerProPheAlaLeuGlnAsnThr 149
DB 925 GACCTCGGCGCTGGGAGATTGTGTGGCTATCGGAGTCCCTCCCTTACGAAACACA 984
QY 150 ValIleThrGlyIleValSerThrAlaGlnArgGlyArgGluLeuGlyLeuArgAsp 169
DB 985 GTTACAAACGGGCTATCTCTCAGCACTGCCAGCGGAGGAGGAGGAGCTGGGCTCCGGGAGC 1044
QY 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro 189
DB 1045 TCCGACATGAGATCAATCCAGAGGATGCCATCATCACTACGGGAACTCCGGGGAGACCA 1104
```

```
QY 190 LeuValAsnLeuAspGlyGlyValIleGlyIleAsnThrLeuLysValIleThrAlaGlyIle 209
DB 1105 CTGGTGAACCTGGAGAGGAGGCTCATTTGGCATCAACAGCTCAAGGTCAAGCTGGGCATTC 1164
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
DB 1165 TCTTTTGGCATCTCCCTCAGACCGGCTACACGGTTCTTCCACAGAGTTCCAAAGACAGCAG 1224
QY 230 IleLysAspTyrLysLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
DB 1225 ATCAAAAGACTGGAAAGACGCTTCATCGGCATACGAGAGCGGACGATCACACAAAGCTTG 1284
QY 250 ValAspGluLeuLysAlaSerAsnProAspPheProGlyValLysSerSerGlyIleThrVal 269
DB 1285 GTGATAGAGCTGAAGGAGCAACCGGACTTCCAGAGGTCCAGCAGTGAATTTATGTG 1344
QY 270 GlnGluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIle 289
DB 1345 CAAGAGGTTCGCCCGAATTCACTTCTCAGAGAGCGGCAATCCAAAGTGTGATCATC 1404
QY 290 ValLysValAsnGlyArgProLeuValAspSerGluLeuGlnGluAlaValLeuThr 309
DB 1405 GTCAAGGTCAACGAGGCGTCTCTAGTGAGCTCGAGTGAGCTGACGAGGCGGTGCTGACC 1464
QY 310 GluSerProLeuLeuLeuGluValAlaArgArgIleAsnAspLeuLeuPheSerIleAla 329
DB 1465 GAGTCTCTCTCTCACTGAGAGGTGCGGCGGAGAACAGCAGCTCTCTTCAGCATCGCA 1524
QY 330 ProGluValAlaMet 334
DB 1525 CCTGAGGTGGTCAATG 1539
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RESULT 7
US-09-818-143-14
Sequence 14, Application US/09818143
Patent No. US20020019000A1
GENERAL INFORMATION:

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APPLICANT: Walker, Michael G.
APPLICANT: Volkmutch, Wayne
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES COEXPRESSED WITH MATRIX-REMODELING GENES
FILE REFERENCE: PB-0004 CIP
CURRENT APPLICATION NUMBER: US/09/818,143
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL Program
SEQ ID NO 14
LENGTH: 2040
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 2814981CBI
US-09-818-143-14
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Alignment Scores:
Pred. No.: 2,31e-175 Length: 2040
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 3 Gaps: 0
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US-10-617-443B-2 (1-334) x US-09-818-143-14 (1-2040)

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QY 10 GlyLeuHISGlnLeuSerSerProArgTyrLysPheAsnPhelLeaAspValValGlu 29
DB 72 GGTCTCCACCAAGCTGAGCAGCCCGCTCAAGTTCACTTCTGTCAGCGTGGAG 131
QY 30 LysIleAlaProAlaValAlaHisIleGluLeuPheLeuArgHisProLeuPheGlyArg 49
DB 132 AAGATCGACCAAGCGGTGTCACATAGAGCTCTTCTGAGACACCGCGGTGTTGGCCG 191
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```

QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
Db 192 AACGTGCCCTGCTCCAGGCGTTCTGGCTTCATCATGTCAGAGGCCGGCTGATCATCAC 251
QY 70 AsnAlaHisValIleSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuIleValGln 89
Db 252 AATGCCCACTGGTGTCCAGCAAGTGTCTGCCCGGCGAGGCAACACACTCAAGGTGAG 311
QY 90 LeuGlnAsnGlyAspSerTrpGluAlaThrIleIleAspIleLeuGlyLeuSerAspIle 109
Db 312 CTACAGAAATGGGAGCTCTCATAGAGCCACCATCAAGACATCGACAGAAAGTCGACAT 371
QY 110 AlaThrIleIleValIleHisProIleValIleValIleProValIleLeuLeuGlyHisSerAla 129
Db 372 GCCACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTGTCTTCTGCTGGTCACTCGGCC 431
QY 130 AspLeuArgProGlyGluPheValIleAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 432 GACCTGCGGCTGGGGAGTTGTGTGGCCATCGGCATCCCTTCGCCCTACAGAACACA 491
QY 150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp 169
Db 492 GTGACAAAGGCGATCTGCAGCACTGCCAGCGGGAGGCGAGGAGCTGGCTTCGGGAGC 551
QY 170 SerAspMetAspTrpIleGlnThrAspAlaIleIleAsnTrpGlyAsnSerGlyGlyPro 189
Db 552 TCCCATCATGACATCATCCAGCGATGCCATCATCACTACGGGAACTCCGGGGAGACA 611
QY 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuIleValIleThrAlaGlyIle 209
Db 612 CTGGTGAACCTGGATGGCGAGGTCTATGGCATCAACGCTCAAGTCACTGGCTGGCATC 671
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspIleGln 229
Db 672 TCCCTTGGCATCCCTCAGACCGCATCAACGCTTCCCAAGAGTTCCAAAGACAAGCAG 731
QY 230 IleIleAspTrpIleValIleArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
Db 732 ATCAAAAGCTGGAAAGAGCGCTTCATCCGCAATCCGATTCGGACATCAACCAAGCCTG 791
QY 250 ValAspGluLeuValIleSerAsnProAspPheProGluValIleSerSerGlyIleTrpVal 269
Db 792 GTGGATGAGCTGAAAGCCAGCAACCGGACTTCCCAAGGTCAAGCATGAAATTTATGCG 851
QY 270 GlnGluValAlaIleProAsnSerProSerGlnArgGlyIleGlnAspGlyAspIleIle 289
Db 852 CAAGAGGTGGCCCAATTCATCTTCAGAGAGCGGCATCCCAAGATGGTGCATCATC 911
QY 290 ValIleValIleAsnGlyArgProLeuValIleAspSerSerGluLeuGlnGluAlaValLeuThr 309
Db 912 GTCAAGGTCAACGGCGCTCTTCTAGTGACTCGAGTGAAGCTGCAAGAGGCCCTGCTGACC 971
QY 310 GluSerProLeuLeuGluValIleArgArgIleAsnAspAspLeuLeuPheSerIleAla 329
Db 972 GAGTCTCCTCTCTCTGAGAGGTGGGGGGGGAACAGACCTCTCTTCAGCATCCCA 1031
QY 330 ProGluValIleMet 334
Db 1032 CCTGAGGTGTCATG 1046

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RESULT 8

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US-10-381-820A-7
; Sequence 7, Application US/10381820A
; Publication No. US2004014233A1
; GENERAL INFORMATION:
; APPLICANT: Deshun, Lu
; APPLICANT: Song, Ho Yeong
; APPLICANT: Su, Eric Men
; APPLICANT: Wang, He
; TITLE OF INVENTION: Novel Secreted Proteins and Their Uses
; FILE REFERENCE: X-13974
; CURRENT APPLICATION NUMBER: US/10/381,820A
; CURRENT FILING DATE: 2003-03-27

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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 2094
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (206)..(1564)
US-10-381-820A-7

Alignment Scores:
Pred. No.: 2.4e-175 Length: 2094
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0
US-10-617-443B-2 (1-334) x US-10-381-820A-7 (1-2094)

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QY 10 GlyLeuHisGlnLeuSerSerProArgTrpIlePheAsnPheIleAlaAspValIleGlu 29
Db 590 GGTCTCCACCAAGCGATGAGCGCCCGCTCAAGATTCACTTCATGTCGAGGTGGAG 649
QY 30 LysIleAlaProAlaValIleHisIleGluPheLeuArgHisProLeuPheGlyArg 49
Db 650 AAGATCGACCAAGCGGTGTCCATAGAGCTTCTCGAGACCCCGCTGTTGGCCGC 709
QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
Db 710 AACGTGCCCTGCTCCAGGCGTTCTGGCTTCATCATGTCAGAGGCCGGCTGATCATCAC 769
QY 70 AsnAlaHisValIleSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuIleValGln 89
Db 770 AATGCCCACTGGTGTCCAGCAAGTGTCTCCCGGCGAGGCAACGCTTACAGGTGAG 829
QY 90 LeuGlnAsnGlyAspSerTrpGluAlaThrIleIleAspIleLeuGlyLeuSerAspIle 109
Db 830 CTACAGAAATGGGAGCTCTCATAGAGCCACATCAAGACATCGACAAAGTCCGACATT 889
QY 110 AlaThrIleIleValIleHisProIleValIleValIleProValIleLeuLeuGlyHisSerAla 129
Db 890 GCCACCATCAAGATCCATCCCAAGAAAAGCTCCCTGTGTCTGCTGGTCACTCGGCC 949
QY 130 AspLeuArgProGlyGluPheValIleAlaIleGlySerProPheAlaLeuGlnAsnThr 149
Db 950 GACCTGCGGCTGGGGAGTTGTGTGGCCATCGGCAGTCCCTTCGCCCTACAGAACACA 1009
QY 150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp 169
Db 1010 GTGACAAAGGCGATCTGCAGCACTGCCAGGGAGGCGAGGAGCTGGCTTCGGGAGC 1069
QY 170 SerAspMetAspTrpIleGlnThrAspAlaIleIleAsnTrpGlyAsnSerGlyGlyPro 189
Db 1070 TCCCATCATGACATCATCCAGGATCCATCATCACTACGGGAACTCCGGGGAGACA 1129
QY 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuIleValIleThrAlaGlyIle 209
Db 1130 CTGGTGAACCTGGATGGCGAGGTCAATGGCATCAACAGCTCAAGTCAACGGCTGGCATC 1189
QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspIleGln 229
Db 1190 TCCCTTGGCATCCCTCAGACCGCATCAACAGGTTCTCCAGAGAGTTCCAAAGACAAGCAG 1249
QY 230 IleIleAspTrpIleValIleArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
Db 1250 ATCAAAAGCTGGAAGAGAGCGCTTCATCGCATTAAGAGTGGGAGATCAACCAAGCCTG 1309
QY 250 ValAspGluLeuValIleSerAsnProAspPheProGluValIleSerSerGlyIleTrpVal 269
Db 1310 GTGGATGAGCTGAAAGCGCAGCAACCGGACTTCCCAAGGTGCACAGCATGGAATTTATGTG 1369

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QY 270 GINGLUVAlA1AProAmsenSerProSerGlnArgGlyYlIeGlnAaspGlyAaspIleIle 289
DB 1370 CAAAGAGTTGGCCGCAATTCACTTCTCAGAGAGGGCGCATCCAGATGGTCAATCATC 1429
QY 290 VALLYSVALA1AProAmsenSerProSerGlnArgGlyYlIeGlnAaspGlyAaspIleIle 309
DB 1430 GTCAAGGTCAAGGGCGGTCTCTAGTGAAGCTCGAGTGAAGTCAAGAGCCGCTGACCC 1489
QY 310 GUSERProLeuLeuLeuGluValAArgAArgGlyAAspAAspLeuLeuPheSerIleAa 329
DB 1490 GAGTCTCTCTCTCTACTGAGGTGCGCGGGAGAACGACGACTCTCTTCAAGCATGCA 1549
QY 330 ProGluValA1Met 334
DB 1550 CCTGAGGTGTCATG 1564

RESULT 9
US-10-956-157-5181
; Sequence 5181, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent version 3.2
; SEQ ID NO 5181
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-5181

Alignment Scores:
Pred. No.: 3,18e-175 Length: 2541
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
Gaps: 0
DB: 9

US-10-617-443B-2 (1-334) x US-10-956-157-5181 (1-2541)

QY 10 GLYLEuHIGlnLeuSerSerProAArgGlyYlIePheAAspPheIleAAspValA1Glu 29
DB 589 GGTCTCCACAGCTGAGCAGCCCGCTCAAGTTCAACTTCATGCTGACGTGTGAG 648
QY 30 LYSILeA1AProA1AValA1HisIleGluLeuPheLeuArgHisProLeuPheGlyArg 49
DB 649 AAGATGGCACCAAGCCGTGTCCATAGAGCTTCTCTAGACACCCGCTGTTGGCCGC 708
QY 50 AAsnValProLeuSerSerGlySerGlyPheIleMetSerGlnA1GlyLeuIleIleThr 69
DB 709 AACGTCCCTGTCGACGAGTCTGCTCATCATGATGACAGAGCCGCGCTGATCATCAC 768
QY 70 AAsnA1HisValA1SerSerAAsnSerA1A1AProGlyAArgGlnIleuLeuValGln 89
DB 769 AATGCCACAGGTGTCTCCAGCAACAGTGTGCTCCCGGACGAGGAGCTCAAGGTGACG 828
QY 90 LeuGlnAAsnGlyAAspSerTyrgIuA1AThrIleLysAAspIleAAspLysLysSerAAspIle 109
DB 829 CTACAGAAATGGGACATCTCTATAGGCCACCATCAAGAGACATGACAGAAAGTCGACATT 888
QY 110 A1AThrIleLysIleHisProLysLysLysLeuProValIleuLeuLeuGlyHisSerA1A 129
DB 889 GCACACATCAAGATCCATCCCAAGAAAGCTCCCTGTGTGTGCTGGGTCACTCGGCC 948
QY 130 AAspLeuArgProGlyYlIeLysPheValA1A1IleGlySerProPheA1A1LeuGlnAAsnThr 149
DB 949 GACCTGGCGCTGGGAGATTGTGTGGCCATCGGACGTCCTCCCTCAAGAACACACA 1008
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QY 150 VALThrThrGlyIleValSerThrA1AglA1nArgGluYlAArgGluLeuGlyLeuAArgAAsp 169
DB 1009 GTGACACGGGCAATGTCATGACACTGCCAGCGGAGGGCAGAGACTGGGCTCCGGGAC 1068
QY 170 SerAAspMetAAspTyrgIleGlnThrAAspA1A1IleAAsnTyrgIyAAsnSerGlyPro 189
DB 1069 TCCGACATGAGACTACATCCAGACGAGTCCATCATCACTACCGGAACTCCGGGGAGACA 1128
QY 190 LeuValA1AAsnLeuAAspGlyGluValI1IleGlyIleAAsnThrLeuLysValThrA1A1Ile 209
DB 1129 CTGTGAACCTGGAATGGAGGTCAATGTGCATCAACAGCTCAAGTCAAGCTGACATC 1188
QY 210 SerPheA1A1IleProSerAAspArgIleThrAArgPheLeuThrGluPheGlnAAspLysGln 229
DB 1189 TCTTTGCCATCCCTTCAGACCGGATCAACGGTTCTTCACAGACTTCAGAGACAGACG 1248
QY 230 I1eLysAAspTyrgLysLysAArgPheI1eGlyIleAArgMetAArgThrIleThrProSerLeu 249
DB 1249 ATCAAAAGACTGGAAAGACGCTTCATCGGCATACGAGATGCGGACGATCACACCAAGCCTG 1308
QY 250 VALAAspGluLeuLysA1ASerAAspProAAspPheProGluValA1SerSerGlyIleTyrgVal 269
DB 1309 GTGATGAGCTGAAGGCGACGACCCGACACTTCCAGAGGTCAAGCATGGAATTATG 1368
QY 270 GINGLUVAlA1AProAmsenSerProSerGlnArgGlyYlIeGlnAaspGlyAaspIleIle 289
DB 1369 CAAAGAGTTGGCCGCAATTCACTTCTCAGAGAGGGCGCATCCAGAAAGTGACATCATC 1428
QY 290 VALLYSVALA1AProAmsenSerProLeuValA1AAspSerGlyLeuGlnGluValA1LeuThr 309
DB 1429 GTCAAGGTCAACGGGCGTCTCTAGTGAAGTCAAGTGAAGTCAAGAGGCGGTGTCAC 1488
QY 310 GUSERProLeuLeuLeuGluValAArgAArgGlyAAspAAspLeuLeuPheSerIleAa 329
DB 1489 GAGTCTCTCTCTCTAGAGGTGCGCGGGAGAACGACGACTCTCTTCAAGCATCCGA 1548
QY 330 ProGluValA1Met 334
DB 1549 CCTGAGGTGTCATG 1563

RESULT 10
US-10-485-313A-31
; Sequence 31, Application US/1048513A
; Publication No. US20050059002A1
; GENERAL INFORMATION:
; APPLICANT: NIE, Guyling
; APPLICANT: SALMONSEN, Lois Adrienne
; APPLICANT: LI, Ying
; APPLICANT: HAMPTON, Anne Lorraine
; APPLICANT: FINDLAY, John Kerr
; TITLE OF INVENTION: Novel Serine Protease
; FILE REFERENCE: 31633-200357
; CURRENT APPLICATION NUMBER: US/10/485,313A
; CURRENT FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: PCT/AU02/01010
; PRIOR FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: PR6707
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent version 3.1
; SEQ ID NO 31
; LENGTH: 2543
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-485-313A-31

Alignment Scores:
Pred. No.: 3,18e-175 Length: 2543
Score: 1635.00 Matches: 325
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 97.4% Indels: 0
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DB: 9 Gaps: 0

US-10-617-443B-2 (1-334) x US-10-485-313A-31 (1-2543)

QY 10 G1YLeuH1sg1nLeuSerSerProArgTyTyTyPheAmpPhe1AlaAspValValGlu 29

Db 577 GGTCTCCACAGACTGAGCAGCCCGGCTACAGAGTTCACTTCATGTCGACGTGTGGAG 636

QY 30 Lys1IleAlaProAlaValValH1st1LeuPheLeuAArgH1ProLeuPheG1Arg 49

Db 637 AAGATCGACCGCCGCTGCTCCATAGAGCTCTTCCGAGACCCCGCTGTTG3CGGC 696

QY 50 AsnValProLeuSerSerG1SerG1Phe1IleMetSerG1AlaG1YLeu1Ile1Thr 69

Db 697 AACGCGCCCTCTCCAGCGGTTCTGCTTCATCATCTCAGAGCCGCGCTGATCTACCC 756

QY 70 AsnAlaH1sValVal1SerSerAAsnSerAlaAlaProG1ArgG1nLeuYValG1n 89

Db 757 AATGCCACGTGCTGTCGACGACAGTGTGCTCCGCGGACGACGACGCTCAAGGTGCAG 816

QY 90 LeuG1nAArg1YAspSerTyTyG1uAlaThr1IleYAsp1IleAsp1YsSerAsp1Ile 109

Db 817 CTACGAATGGGAGCTCTATAGAGCCACCATCAAGACATCGACAAAGTCGAGACAT 876

QY 110 AlaThr1IleYs1IleH1sProYs1Ys1YsLeuProVal1LeuLeuG1YH1sSerAla 129

Db 877 GCCACCATCAAGATCTCATCCCAAGAAAAGCTCCCTGTTCTTGTGCTGCTGCTGCTG 936

QY 130 AspLeuArgProG1YG1uPheValValAla1IleG1YSerProPheAlaLeuG1nAAsnThr 149

Db 937 GACCTCGGCTGGGAGATTTGTGTGTCGACATCGGACATCCCTTCCCTTACAGAACCA 996

QY 150 Val1Thr1nG1Y1IleVal1SerThrAlaG1nArgG1uG1YArgG1uLeuG1YLeuArgAsp 169

Db 997 GTGAAACGGGATCTGTGACGCTGCCAGCGGAGGAGGAGGAGCTGGGCTCCGGGAGC 1056

QY 170 SerAspMetAspTyTy1IleG1nThrAspAla1Ile1AsnTyTyG1YAsnSerG1YG1Pro 189

Db 1057 TCCGACATGAGCTACATCCAGCGATGCTCATCATCACTACGAGAACTCCGGGGAGCA 1116

QY 190 LeuValAAsnLeuAspG1YG1uVal1IleG1Y1IleAAsnThrLeuYVal1ThrAlaG1Y1Ile 209

Db 1117 CTGGGACATCGATGAGGAGGATGATGTCATCAACAGCTCAAGGTCAAGGCTGGCATC 1176

QY 210 SerPheAla1IleProSerAspArg1IleThrArgPheLeuThrG1uPheG1nAsp1YsG1n 229

Db 1177 TCTTTTGCATCTCCCTCAGACCGCATCAACGCTTCTCCACAGAGTTCCAAAGACAGCAG 1236

QY 230 IleYsAspTyTyP1YsArgPhe1IleG1Y1IleArgMetArgThr1IleThrProSerLeu 249

Db 1237 ATCAAGACATGAGAGAGAGGCTTCATCGGCATACGAGATGCGGACCATCAACCAAGCCTG 1296

QY 250 ValAspG1uLeuYsAla1SerAAsnProAspPheProG1uVal1SerSerG1Y1IleTyVal 269

Db 1297 GTGATGAGCTGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1356

QY 270 G1nG1uValAla1ProAsnSerProSerG1nArgG1YG1Y1IleG1nAspG1YAsp1Ile1Ile 289

Db 1357 CAAGAGGTTGGCCCAATTCACCTTCTCAGAGAGCGGAGTCAGAGATGTGTGACATCATC 1416

QY 290 ValYsValAAsnG1YArgProLeuValAAspSerSerG1uLeuG1nG1uAlaVal1LeuThr 309

Db 1417 GTCAAGGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1476

QY 310 G1uSerProLeuLeuG1uVal1ArgArgG1YAsnAspAspLeuPheSer1IleAla 329

Db 1477 GAGTCT 1536

QY 330 ProG1uValValMet 334

Db 1537 CCTGAGGTGTCTATG 1551

RESULT 11

US-09-796-753-31

Sequence 31, Application US/09796753

Publication No. US20030027998A1

GENERAL INFORMATION:

APPLICANT: McCarthy, Sean A.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

FILE REFERENCE: 7853-227-999

CURRENT APPLICATION NUMBER: US/09/796,753

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 09/183,175

PRIOR FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/223,094

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/223,546

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/224,246

PRIOR FILING DATE: 1998-12-30

PRIOR APPLICATION NUMBER: 09/259,388

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/122,458

PRIOR FILING DATE: 1999-03-01

PRIOR APPLICATION NUMBER: 09/312,359

PRIOR FILING DATE: 1999-05-14

PRIOR APPLICATION NUMBER: 09/336,536

PRIOR FILING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 09/342,687

PRIOR FILING DATE: 1999-06-29

PRIOR APPLICATION NUMBER: 09/345,464

PRIOR FILING DATE: 1999-06-30

PRIOR APPLICATION NUMBER: 09/365,164

PRIOR FILING DATE: 1999-07-30

PRIOR APPLICATION NUMBER: 09/399,723

PRIOR FILING DATE: 1999-09-20

PRIOR APPLICATION NUMBER: 09/409,634

PRIOR FILING DATE: 1999-09-30

PRIOR APPLICATION NUMBER: 09/471,179

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 09/474,071

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/474,072

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/514,010

PRIOR FILING DATE: 2000-02-25

PRIOR APPLICATION NUMBER: 09/516,745

PRIOR FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: 09/572,002

PRIOR FILING DATE: 2000-05-14

PRIOR APPLICATION NUMBER: 09/597,993

PRIOR FILING DATE: 2000-06-19

PRIOR APPLICATION NUMBER: 09/559,596

PRIOR FILING DATE: 2000-06-22

PRIOR APPLICATION NUMBER: 09/630,334

PRIOR FILING DATE: 2000-07-31

PRIOR APPLICATION NUMBER: 09/606,565

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: 09/606,317

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: 09/665,666

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: 09/677,751

PRIOR FILING DATE: 2000-09-30

NUMBER OF SEQ ID NOS: 162

SEQ ID NO 31

LENGTH: 2576

TYPE: DNA

ORGANISM: Homo sapiens

US-09-796-753-31

Alignment Scores:

Pred. No.: 3,24e-175

Score: 1635.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Length: 2576

Matches: 325

Conservative: 0

Mismatches: 0

Query Match: 97.4% Indels: 0
DB: 3 Gaps: 0
US-10-617-443b-2 (1-334) x US-09-796-753-31 (1-2576)

DB 10 G1YLeuH1eGlnLeuSerSerProArGTYrLySPheAnPhe1leAlaAPVa1ValG1u 29
DB 606 GGCTTCACACGCTGAGCGCCGCGCTCAAGTTCAACTTCATGCTGAGCTGGTGAG 665
DB 30 Lys1leAlaProAlaValAlaH1eG1uLeuPheLeuXHis1ProLeuPheG1yArg 49
DB 666 AAGATCGACCGACCGGTGTCCACATAGAGCTTCTCTGAGACACCGCGTGTGGCGCG 725
DB 50 AenVal1ProLeuSerSerG1ySerG1yPhe1leMeSerG1uAlaG1yLeu1le1eThr 69
DB 726 AACGTGCCCCCTGTCACGCGGTTCCTTCATCATATGTCAGAGCCGCGCTGATCATACC 785
DB 70 AenAlaH1eVal1Val1SerSerAenSerAlaAlaProG1yArgG1nG1nLeu1yValG1n 89
DB 786 AATGCCCACTGGTGTTCAGCAACATGCTGCCCGCGGACGACGACGCTCAAGGTGACG 845
DB 90 LeuG1nAenG1yAAsperTYrG1uAlaThr1le1yAAsp1leAAsp1y1ySerAAsp1le 109
DB 846 CTACAGATGGGAGCTCTATGAGCCACCATCAAGACATGACAAAGATCGACATT 905
DB 110 AlaThr1le1yAl1eH1eSProLYbLYLeuProVal1leuLeuG1yH1eSerAla 129
DB 906 GCCACCATCAAGATCCATCCCAAGAAAGCTCCCTGTGTGTGCTGGGTCACTCGGCC 965
DB 130 AAspLeuArgProG1yG1uPheVal1Ala1leG1ySerProPheAlaLeuG1nAenThr 149
DB 966 GACCTGGCGCTGGGAGTTGTGTGGTCCATCGGACGTCCTTCGCTACAGAAACAC 1025
DB 150 Val1Thr1le1y1leVal1SerThrAlaG1nArgG1uG1yArgG1uLeuG1yLeuAAsp 169
DB 1026 GTGCAACGGGCACTGTGACGACCTGCCAGGGAGGGACGAGGCTGGGCTCCGGGAG 1085
DB 170 SerAAspMeAAspTYr1leG1nThrAAspAla1le1leAenTYrG1yAAsnSerG1yG1yPro 189
DB 1086 TCCGACATGAGCTATCATCCAGACGAGTCCCATCATCACTACAGGAACTCCGGGGAGCA 1145
DB 190 LeuVal1AenLeuAAspG1yG1uVal1leG1y1leAenThrLeu1yVal1ThrAlaG1y1le 209
DB 1146 CTGGTGAACCTGTAGGAGGTATGGCATCAACAGCTCAAGGTCAACGCGCTGGCATC 1205
DB 210 SerPheAla1leProSerAAspArg1leThrArgPheLeuThrG1uPheG1nAAspLYeG1n 229
DB 1206 TCTCTTGGCATCCCTCTGACGACCGCATCAACGTTCTCAAGAGTTCCAAAGACAG 1265
DB 230 1le1yAAspTYrLYbLYbArgPhe1leG1y1leArgMe1ArgThr1leThrProSer1eU 249
DB 1266 ATCAAGAGCTGGAAGAGACGCTTCATCGGCATACGAGATGGAGCATCAACAGCTG 1325
DB 250 Val1ePheG1uLeu1yAlaSerAAspProAAspPheProG1uVal1SerSerG1y1leTYrVal 269
DB 1366 GTGATGAGCTGAGAGCGACGACGACGACTTCCAGAGGTCAAGAGTGAATTATATGTG 1385
DB 270 G1nG1uVal1AlaProAAsnSerProSerG1nArgG1yG1y1leG1nAAspG1yAAsp1le1le 289
DB 1386 CAAAGAGTTGGCGCAATTCACCTTCTCAAGAGCGGCAATCCAAAGATGGAGCATCTC 1445
DB 290 Val1yVal1AenG1yArgProLeuVal1AAspSerSerG1uLeuG1nG1uAlaVal1leuThr 309
DB 1446 GTCAAGGTTCACGGGCGTCTCTTATGATCATGATGAGCTGCAAGAGCGCGTGTGACC 1505
DB 310 G1uSerProLeuLeuG1uVal1ArgArgG1yAAsnAAspAAspLeuPheSer1leAla 329
DB 1506 GAGTCTCTCTCTCTATGAGAGGTGGCGGGGAAAGCAAGACCTCTCTTCAAGCATCGCA 1565
DB 330 ProG1uVal1ValMet 334
DB 1566 CCTGAGGTGTGATG 1580

RESULT 12
US-10-485-313A-26
Sequence 26, Application US/10485313A
Publication No. US20050059002A1
GENERAL INFORMATION:
APPLICANT: NIT, Guiying
APPLICANT: SALAMONSEN, Lois Adrienne
APPLICANT: LI, Ying
APPLICANT: HAMPTON, Anne Lorraine
APPLICANT: FINDLAY, John Kerr
TITLE OF INVENTION: Novel Serine Protease
FILE REFERENCE: 31633-200357
CURRENT APPLICATION NUMBER: US/10/485,313A
PRIOR FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: PCT/AU02/01010
PRIOR FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: PR6707
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ. ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 2450
TYPE: DNA
ORGANISM: Mus musculus
US-10-485-313A-26

Alignment Scores:
Pred. No.: 5.75e-164 Length: 2450
Score: 1536.00 Matches: 302
Percent Similarity: 96.6% Conservative: 13
Best Local Similarity: 92.6% Mismatches: 0
Query Match: 91.5% Indels: 0
Gaps: 0
DB: 9

US-10-617-443b-2 (1-334) x US-10-485-313A-26 (1-2450)

DB 9 AlaG1yLeuH1eGlnLeuSerSerProArGTYrLySPheAnPhe1leAlaAPVa1Val 28
DB 526 TCTGGTTCACACGCTGAGCGATCGCGGTACAAAGTTCACTTCATGCGGATGTG 585
DB 29 G1uYs1leAlaProAlaValAlaH1eG1uLeuPheLeuAAsp1leProLeuPheG1y 48
DB 586 GAGAAATGGCCGCGCTGTGTGTCCATAGAGCTTTCGAGACACCCCTGTTGGC 645
DB 49 ArgAenVal1ProLeuSerSerG1ySerG1yPhe1leMeSerG1uAlaG1yLeu1le1e 68
DB 646 CGGAATGTCCGCTGTCAGGTGGCTTCATCATGTCAAGAGCCGTTGATCGTC 705
DB 69 ThrAenAlaH1eVal1Val1SerSerAenSerAlaAlaProG1yArgG1nG1nLeu1yVal 88
DB 706 ACCAAGCCGACGTTGTCTTCAGCTCCAGCTCCGCTCCGCGGACGACGCTGAAGGTG 765
DB 89 G1nLeuG1nAenG1yAAsperTYrG1uAlaThr1le1yAAsp1leAAsp1y1ySerAAsp 108
DB 766 CAGCTCAAGATCGGATGCTTATGAGGCGCACATCCAGAGATCGACAAAGTCCGAC 825
DB 109 1leAlaThr1le1yAl1eSProLYbLYbArgPhe1leG1y1leArgMe1ArgThr1leThr 128
DB 826 ATGCAAGATGTATATCCACCCCAAGAAAGCTCTCTGTGTGCTGCTGCTGCTCACTCA 885
DB 129 AlaAAspLeuArgProG1yG1uPheVal1Ala1leG1ySerProPheAlaLeuG1nAAsn 148
DB 886 GCAAGACTGGCGGCTGCGCAAGTTCTGTGTGGCATGGGACGCGCTTCCCTGCAGAAC 945
DB 149 ThrVal1ThrThrG1y1leVal1SerThrAlaG1nArgG1uG1yArgG1uLeuG1yLeuAAsp 168
DB 946 ACCGTGCAACGGGCAATTCACGACCTGCCACGCGGAGTGGCAAGAGCTGGGTCTCCG 1005
DB 169 AAspSerAAspMeAAspTYr1leG1nThrAAspAla1le1leAAspTYrG1yAAsnSerG1yG1y 188
DB 1006 GACTCAGACATGAGCTATATCCAGACCGATGCGCATCATCAATTACGGGAATCAGAGAGA 1065
DB 189 ProLeuVal1AenLeuAAspG1yG1uVal1leG1y1leAenThrLeu1yVal1ThrAlaG1y 208


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US-09-764-898-112
; Sequence 112, Application US/09764898
; Patent No. US2002090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ201
; CURRENT APPLICATION NUMBER: US/09/764,898
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 112
; LENGTH: 1868
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-898-112

Alignment Scores:
Pred. No.: 3, 91e-146 Length: 1868
Score: 1378.00 Matches: 275
Percent Similarity: 98.6% Conservative: 0
Best Local Similarity: 98.6% Mismatches: 4
Query Match: 82.1% Indels: 0
DB: 3 Gaps: 0

US-10-617-443b-2 (1-334) x US-09-764-898-112 (1-1868)

QY 56 GlySerGlyPheIleMetSerGluAlaGlyLeuIleGlyThrAsnAlaHisValSer 75
DB 23 GGTTCGGCTTCATCATGTAGAGGCGGCTCATCATCCAAATGCCACGGTGTCTC 82
QY 76 SerAsnSerAlaAlaProGlyArgGlnGlnLeuIleValGlnLeuGlnAsnGlyAspSer 95
DB 83 AGCAACAGTCTGACGCCGCGGACGACGCTCAAGGTGCGATGCAATGCGGACTCC 142
QY 96 TyrGluAlaThrIleLeuAspIleAspIleAspIleAspIleAspIleAspIle 115
DB 143 TATGAGGCCACCAATCAAGACATCGACAAAGATGCGACATGCAATCAAGATCAT 202
QY 116 ProIleValLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGlu 135
DB 203 CCCAAGAAAGCTCCCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 262
QY 136 PheValAlaAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIleVal 155
DB 263 TTGTGTGGTGGCATCGGACATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 322
QY 156 SerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrIle 175
DB 323 AGCATCGCCACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 382
QY 176 GlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyProLeuValAsnLeuAspGly 195
DB 383 CAGAGGATGCGCATCATCACTACGCGGAATCCGCGGAGCACTGCGGAACCTGATGCG 442
QY 196 GluValIleGlyIleAsnThrLeuIleValThrAlaGlyIleSerPheAlaIleProSer 215
DB 443 GAGGTGATGGCATCAACAGCTCAAGGCTCAAGGCTGAGCTCTCTTGTGCAATCCCTCA 502
QY 216 AspArgIleThrArgPheLeuThrGluPheGlnAspIleGlyAspTyrIleVal 235
DB 503 GACCCGATCAACAGGTTCTCAAGAGTTCCAAAGCAAGCATCAAGATCGGAAGAG 562
QY 236 ArgPheIleGlyIleArgMetArgThrIleThrProSerLeuValAspGluLeuValAla 255
DB 563 CGCTTCATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 622
QY 256 SerAsnProAspPheProGluValSerSerGlyIleTyrValGlnGluValAlaProAsn 275
DB 623 AGCAACCCGAGACTTCCCAAGGTCAAGCATGGAATTTATGTGCAAGAGGTTGCGCGAAT 682
QY 276 SerProSerGlnArgGlyIleGlnAspGlyAspIleIleValIleValAsnGlyArg 295
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DB 683 TCACTTCTCAGAGAGCGGATCCAAAGATGAGATCATGCTCAAGGTCAACGGGCGT 742
QY 296 ProLeuValAspSerSerGluLeuGlnGluValIleValLeuThrGluSerProLeuLeu 315
DB 743 CCTTATGAGACTCGAGTGAAGTGCAGAGGCGGTCTGACCAAGTCTCTCTCTACTG 802
QY 316 GluValArgArgGlyAsnAspAspLeuPheSerIleAlaProGluValAlaMet 334
DB 803 GAGGTGCGGCGGAGCAAGCACTCTTTCAGCATGCGACACTGAGTGTGATG 859

RESULT 15
US-09-969-384-7
; Sequence 7, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT055P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-969-384-7

Alignment Scores:
Pred. No.: 5, 02e-117 Length: 1695
Score: 1122.00 Matches: 243
Percent Similarity: 80.3% Conservative: 13
Best Local Similarity: 76.2% Mismatches: 33
Query Match: 66.8% Indels: 30
DB: 3 Gaps: 6

US-10-617-443b-2 (1-334) x US-09-969-384-7 (1-1695)

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DB 229 GGTTCACACCACTGAGGAGCGCGCTCAAGTTCAATTCATGCTGACGCTGTGGAG 288
QY 30 LysIleAlaProAlaValAlaHisIleGluLeuPheLeuArgHisProLeuPheGlyArg 49
DB 289 AAGATGCAACAGCCGTGTGCAATAGAGCTCTTCTGAGCAACCGCTGTTGGCCGC 348
QY 50 AsnValProLeuSerSerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThr 69
DB 349 AACGTCCCTGCTGCAAGGCTTCTGCTTCATCATGATGAGAGCGCGCTGATCATACC 408
QY 70 AsnAlaHisValAlaSerSerAsnSerAlaAlaProGlyArgGlnGlnLeuIleValGln 89
DB 409 AATGCCACAGTGGTGTCCAGCAACAGTGTGCCCCCGGAGGAGGAGGAGGAGGAGGAG 468
QY 90 LeuGlnAsnGlyValAspSerTyrGluAlaThrIleLeuAspIleAspIleValSerAspIle 109
DB 469 CTACAGAAATGGGACTCTCTATGAGGCGACCATCAAGACATGACAAAGTCGACATT 528
QY 110 AlaThrIleLysIleHisProLysIleValLeuProValLeuLeuGlyHisSerAla 129
DB 529 GCCACATCAAGATTCATCCCAAGAAAGAGCTCCGTGTGTGTGCTGCGGTCACTGGCC 568
QY 130 AspLeuArgProGlyGluPheValAlaAlaIleGlySerProPheAlaLeuGlnAsnThr 149
DB 589 GACCTGGCGCTGGGAGATTGTGTGGCCATGCGAGTCCCTTCCGCTCAAGAACACA 648
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Qy 150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAsp 169
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Qy 170 SerAspMetAspTyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyPro 189
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Db 709 TCCGACATGACATCACTACAGCGGATCCATCACTACAGGGAATCCGGGGGACCA 768
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Qy 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuValThrAlaGlyIle 209
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Db 769 CTGGTGAACCTGGATGGCGAGTCAATTGGCATCAACAGCTCAAGTCAAGCTGGCATC 828
    |||||
Qy 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
    |||||
Db 829 TCTTTGGCATCCCTTCAGACCGCATCAACGGTTCTTCACAGAGTTCAGAGACAGCAG 888
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Qy 230 IleLysAspTyrPylsArgPheIleGlyIleArgMetArgThrIleThrProSerLeu 249
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Db 889 ATCAAA-----GCCCTCACTG 906
    |||||
Qy 250 ---ValAspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyr 268
    |||||
Db 907 GCAGTTCATTGAGAGCAGGGGCTTCTCAAGTTCCCTTCCTCCATGACCCCTCAGC 966
    |||||
Qy 269 ValGlnGluValAlaProAsnSerPro-----SerGlnArg 280
    |||||
Db 967 CAAACACATKADACCCCGTGCAGCCAGCCAGGCTGGTCCATGAGGGCTGTGCATGAAGA 1026
    |||||
Qy 281 GlyIleIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeu---ValAsp 299
    |||||
Db 1027 GCTGCTGTGAGAGATGCCGCAATTGTTCTCTGTGT-----CCATTATGGGAAGAC 1077
    |||||
Qy 300 SerSerGluLeuGlnGlnGluAlaValLeuThrGlu-----SerProLeuLeuLeu 315
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Db 1078 AATCTGAGCGCAGGCGAGCTGTCTTTCCTCAAGAAAGCTGAAGTCTTCTCTTGG 1134
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Job time : 839 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: February 21, 2006, 20:57:05 ; Search time 495 Seconds

(without alignments)
1432.363 Million cell updates/sec

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Perfect score: 1679
Sequence: 1 MHLALPASAGLHQLSSPRK.....LEVRGNDLLFSTAPEVVM 334

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Ygapop 10.0, Ygapext 0.5	
Fgapop 6.0, Fgapext 7.0	
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Searched: 7204323 seqs, 1061406715 residues

Total number of hits satisfying chosen parameters: 14408646

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPT=0 -LOOPTXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Published Applications NA New:*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1482.5	88.3	2551	12	US-11-186-284-78
2	1034.5	61.6	1443	8	US-10-821-234-613
3	1034.5	61.6	1894	9	US-11-072-512-795
4	1034.5	61.6	2036	12	US-11-091-883-91

5 882 52.5 2476 12 US-11-183-914-23 Sequence 23, Appl
6 414 24.7 1497 8 US-10-467-657-2095 Sequence 2095, Ap
7 410 24.4 1425 12 US-11-098-686-9246 Sequence 9246, Ap
8 410 24.4 1457619 12 US-11-098-686-8739 Sequence 8739, Ap
9 360.5 21.5 1446 8 US-10-454-437-55 Sequence 55, Appl
10 347 20.7 3007 8 US-10-793-626-3848 Sequence 3848, Ap
11 347 20.7 3650 8 US-10-793-626-3756 Sequence 3756, Ap
12 335.5 20.0 1269 12 US-11-074-176-3 Sequence 3, Appl
13 318 18.9 954 8 US-10-793-626-1823 Sequence 1823, Ap
14 282 16.8 908 8 US-10-750-185-32084 Sequence 32084, A
15 282 16.8 908 8 US-10-750-623-32084 Sequence 32084, A
16 260.5 15.5 1482 8 US-10-793-626-1831 Sequence 1831, Ap
17 260.5 15.5 3794 8 US-10-793-626-3705 Sequence 3705, Ap
18 230.5 13.7 4301 8 US-10-793-626-3538 Sequence 3538, Ap
19 192 11.4 3106 8 US-10-793-626-4209 Sequence 4209, Ap
20 162 9.6 1376 8 US-10-750-185-32073 Sequence 32073, A
21 162 9.6 1376 8 US-10-750-623-32073 Sequence 32073, A
22 143 8.5 200 12 US-11-098-686-3608 Sequence 3608, Ap
23 131.5 7.8 200 12 US-11-098-686-3609 Sequence 3609, Ap
24 128 7.6 1314 8 US-10-454-437-59 Sequence 59, Appl
25 122 7.3 3343 8 US-10-485-517-31 Sequence 31, Appl
26 117.5 7.0 2033 8 US-10-485-517-32 Sequence 32, Appl
27 117 7.0 1102 8 US-10-750-185-32074 Sequence 32074, A
28 117 7.0 1102 8 US-10-750-623-32074 Sequence 32074, A
29 115.5 6.9 2806 8 US-10-485-517-30 Sequence 30, Appl
30 110.5 6.6 6582 12 US-11-000-688-606 Sequence 606, Ap
31 105 6.3 8575 8 US-10-453-372-167 Sequence 167, Ap
32 103 6.1 1944 8 US-10-793-626-567 Sequence 567, Ap
33 103 6.1 3073 8 US-10-793-626-3483 Sequence 3483, Ap
34 103 6.1 3353 8 US-10-793-626-3481 Sequence 3481, Ap
35 100.5 6.0 1422 8 US-10-467-657-5917 Sequence 5917, Ap
36 100.5 6.0 1422 8 US-10-467-657-7517 Sequence 7517, Ap
37 100 6.0 14770 8 US-10-821-234-268 Sequence 268, Ap
38 99.5 5.9 849 8 US-10-793-626-363 Sequence 363, Ap
39 99.5 5.9 3189 8 US-10-793-626-3694 Sequence 3694, Ap
40 99 5.8 1283 8 US-10-821-234-348 Sequence 348, Ap
41 97.5 5.8 1329 12 US-11-098-686-10023 Sequence 10023, A
42 96.5 5.7 1809 8 US-10-467-657-5017 Sequence 5017, A
43 93 5.5 6999 8 US-10-453-372-169 Sequence 169, Ap
44 93 5.5 8160 8 US-10-453-372-113 Sequence 113, Ap
45 93 5.5 9668 8 US-10-453-372-135 Sequence 135, Ap

ALIGNMENTS

RESULT 1
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; Sequence 78, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamathkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgate, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228

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	;	SEQ ID NO: 78	
	;	LENGTH: 2551	
	;	TYPE: DNA	
	;	ORGANISM: Homo Sapiens	
	;	FEATURE:	
	;	NAME/KEY: CDS	
	;	LOCATION: (1222)...(1580)	
	US-11-186-284-78		
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	Pred. No.:	5.17e-168	Length: 2551
	Score:	1482.50	Matches: 319
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	Best Local Similarity:	97.6%	Mismatches: 6
	Query Match:	86.3%	Indels: 7
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DB	606	GGCTTCACACAGTGTAGACAGCCCGGCTCAAGTTCATTCATGTGACGTGTGGAG	6655
QY	30	LYSIIIEALAPROALAVAIValINIIEGLIULEUPHEUARYHISPRoleuphegiYArg	49
DB	666	AAAGATGCACACAGCCGTGTGCCATATAGAGCTCTTCTTGAGACACCCGCTTTGGCCGC	7255
QY	50	AAAPAVALPoleuSERserGIYserGIYpHEIImetSERCIuIAgiYLEuIIEIIEthr	69
DB	726	AAAGTCCCTCTGTCCAGCGGTTCTGCTTCATCATGTCAAGAGCGCGCTGATCATCAC	7855
QY	70	AAAPALHIEIAVALSERSERAAENSERALAIAPROGIYARGINGIULEUYSVALG	89
DB	786	AAATGCCACATGGTGTGCCAGCAACATGCTGCCCGGCGAGGACAGCATCAAGTGTGAC	8455
QY	90	LEUGINAEAGLYAASPSERTYRGUAIATHTIIELYAHAPLIEAPLYVLYSERAPPIE	1095
DB	846	CTACAGAAATGGGACCTCTATAGAGCCACCATCAAGACATCAAGAAAGTCGCATT	9055
QY	110	AIATHTIIELYNIIEHISPRoLYSLVLYLEUPROVALIIEUHEUENUGIYHISERAla	1295
DB	906	GCCACCATCAAGTCCATCCCAAGAAAGACCTCCCTGTGTGTGCTGGGTACTCGGCC	9655
QY	130	AAPLIEUARYPROGIYGIUHPHEVALVAlAIEGLIYserPROBheIAleuGINAenThr	1495
DB	966	GACCTGCGCGGT-GGGGAGTTTGGGGGCGCATCGGAGT-CCCTTCGCCCTACAGAAACA	1020
QY	150	VALITHTTHGILIEVALSERTHRIAGINAGGIUGLIYARGGIULEUGIYLEUARYAASP	1695
DB	1024	GTGACAC-GGCACTGCT-AGCACTGCCAGCG-GAGGGCAGGAGCGTGGCCCTCCGGAC	1080
QY	170	SEAAPEMETASPTYLIE-GIINTHRAPALAIIEIE-AAHYRGIIYAHSERGIYIYP	1895
DB	1081	TCCGACATGAGCTACATCAACAGCGATGTCATCATCAACTCAAGGAACTCGGGGGAC	1140
QY	188	ROLEUVALIENLEUAPGIYGIUVALIIEGLIYLEAenTHRIEULYVALTHAlAGIYI	2095
DB	1141	CACCTGGTGAACCTGTGATGGCGAGGTATATGGCATCAACGCTCAAGAGTCAACGCTGGCA	1200
QY	209	IESERPhEAlIIEPRosERASPAIGLIETHXARGPHEIUTHRGIUPHGIASPLYSG	2295
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QY	228	IIIEIYASPTPIYSLYSLARGPHEIIEGLIYLEARGHETARGTHRIETHPROSERL	2495
DB	1261	AGATCAAAAGACTGTAAAGAACGCTTCATCGGCATAGCGATGCGGACGATCAACCAAGCC	1320
QY	249	EUVALIASPGLIUEUYSALIASERASPAHPHEPROGIUVALISERSEGLIIEHYV	2695
DB	1321	TGTGTGATAGCTGAAGGCCACGACACCCGGACTTCCAGAGGTCAGAGTGGGAATTTATG	1380
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Db	1381	TGCAAGAGTTGGCCGAATTCACTTCTCAGAGAGGGCGCATCCAGATGTGATCTCA	1443			
Qy	289	leVallybVaJaengIyArProeuVaJaSpSerSerGluLeuGlnGluAlaValleut	309			
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Qy	309	hrgIuserProleuLeuLeuGluValAlaArgGlyAAspAspLeuLeuPheSerIleA	328			
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; Publication No. US20050255114A1						
; GENERAL INFORMATION:						
; APPLICANT: Labat, Ivan						
; APPLICANT: Seache-Crain, Birtic						
; APPLICANT: Andarmann, Susan						
; APPLICANT: Tang, Y. Tom						
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia						
; FILE REFERENCE: 821A						
; CURRENT APPLICATION NUMBER: US/10/821,234						
; PRIOR FILING DATE: 2004-04-07						
; PRIOR APPLICATION NUMBER: US 60/462,047						
; PRIOR FILING DATE: 2003-04-07						
; NUMBER OF SEQ ID NOS: 1704						
; SOFTWARE: pc_seq_genes Version 1.0						
; SEQ ID NO 613						
; LENGTH: 1443						
; TYPE: DNA						
; ORGANISM: Homo sapiens						
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Qy	24	lIeAlAAspVaIyAlGluIySerIleAlaProAlaValAlaHisIleGluLeuPheLeuArg	43			
Db	514	ATGGCGGAGCGTGTGAGAAAGATCCCGCTCGGTGATTATCGAATTGTTTCGCAAG	573			
Qy	44	HiAProLeuPheGlyArqAsnValProLeuSerSerGlySerGlyPheIleMetSerGlu	63			
Db	574	CTTCCGTTTCTTAACAGAGAGGTGCCGGGTGCTGTGGTATATGTCGAA	633			
Qy	64	AlAGlyLeuIleIleThrAsnAlaHisValValSerSerAsnSerAlaAlaProGlyArg	83			
Db	634	GATGGACTATCTGTGCAAAATCCACCTGTGTGACCAAC-----AAG	675			
Qy	84	GlnGlnLeuLybValGlnLeuGlnAsnGlyAspSerTyrgIuaIathrIleLybAspIle	103			
Db	676	CACCGGCTCAAAAGTTAGCTGAAGAACGGTGCACCTTACGAAGCCAAATCAAGAGTGTG	735			
Qy	104	AspLybLybSerAspIleAlaThrIleLybIleHisProLybLybLybLeuProValLeu	123			
Db	736	GATGAGAAAGACACACTGCCACTCATCAAAATATGACACAGGCGCAAGCTGCTGTCCTG	795			
Qy	124	LeuLeuGlyHisSerAlaAspLeuArgrProGlyGlnPheValAlaIleGlySerPro	143			

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Db      796 CTGCTGGCCGCTCTCAGAGCTGGCGGAGAGTTGTTGTCGCATCGGAAGCCCG 855
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Qy      204 LysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
Db      1036 AAAGTGACAGCTGATCTCTTCCAAATCCCATCTGATTAAGATTAAAGTTCTCTCAG 1095
Qy      224 GluPheGlnAspLysGlnIleLysAsp-----TPrlyLeuArgPheIleGlyIle 240
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Qy      241 ArgMetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAspHe 260
Db      1156 CGAATGATGTCTACTACGTCGACGCAAGCAAGCAAGCTGAAGAGACCGGACCGGACTTC 1215
Qy      261 ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg 280
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Qy      281 GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer 300
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Qy      301 SerGluLeuGlnGluAlaValLeuThrGlnSerProLeuLeuGluValAlaArgArgGly 320
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Qy      321 AsnAspAspLeuLeuPheSerIleAlaProGluValVal 333
Db      1396 AATGAATATCATCATGATCAAGTGAATCCCGAAGAAATT 1434

RESULT 3
US-11-072-512-795
; Sequence 795, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YORI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTOKU
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072, 512
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350, 978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379296

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; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 795
; LENGTH: 1894
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-795

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Pred. No.: 3,89e-114 Length: 1894
Score: 1034.50 Matches: 206
Percent Similarity: 80.2% Conservative: 61
Best Local Similarity: 61.9% Mismatches: 57
Query Match: 61.6% Indels: 10
DB: 9 Gaps: 2

US-10-617-443B-2 (1-334) x US-11-072-512-795 (1-1894)

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Db      358 GCGAGCCTGGCGGCGCAAGGCGAG-GAAGATCCCAACTTTGGCCATTAATATTAATTTT 416
Qy      24 IleAlaAspValAlaGluLysIleAlaProAlaValAlaHisIleGluLeuPheLeuArg 43
Db      417 ATCCGGAGCGTGTGAGAGAAAGATGCGCCCTCCGCGTTCAATATGAAATTGTTGCGAAG 476
Qy      44 HisProLeuPheGlyArgAsnValProLeuSerSerGlySerGlyPheIleMetSerGlu 63
Db      477 CTTCGGTTTCTTAAACGAGAGGTGCGGTGCTAGTGTGGTATGTGGTTATTTGTGCGAA 536
Qy      64 AlaGlyLeuIleIleThrAsnAlaHisValValSerSerAsnSerAlaAlaProGlyArg 83
Db      537 GATGACATGATGTGACAAATGCCCCACGTGTGACCAAC-----AAG 578
Qy      84 GlnGlnLeuLysValGlnLeuGlnAsnGlyAspSerTyrGlnAlaThrIleLysAspIle 103
Db      579 CACCGGTCMAAGTTGACTGAGAGACGATGCGCACTTGCAAGCCAAATCAAGATGTG 638
Qy      104 AspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLysLeuProValLeu 123
Db      639 GATGAAAGACGACATGCACTCAATAATTGACCAACGAGGCACTGCTGTCTCG 698
Qy      124 LeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValAlaIleGlySerPro 143
Db      699 CTGCTGGCCGCTCTCAGAGCTGGCGGAGAGTTGTTGTCGCATCGGAAGCCCG 758
Qy      144 PhealaleuGlnAenThValThrThrglylleValSerThrAlaGlnArgGluGlyArg 163
Db      759 TTTTCCCTTCAAAACACAGCTCCACCGGATCGTAGACACCAACCGAGCGGCGCAAA 818
Qy      164 GluLeuGlyLeuArgAspSerSerPheTyrIleGlnThrAspAlaIleIleAsnThr 183
Db      819 GAGCTGGGGCTCCGCACTCAGACATGACTACATCCAGACGACCGCATCTCAACTAT 878
Qy      184 GlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeu 203
Db      879 GGAACCTGGGAGCGCCGTTAGTAAACCTGACGCGTAGATGAAATTAATTAACCTTTG 938
Qy      204 LysValThrAlaGlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThr 223
Db      939 AAAGTGAAGCTGGAATCTCTTTCATCCCATCTGATTAAGATTAAAGTTCTCTCAG 998
Qy      224 GluPheGlnAspLysGlnIleLysAsp-----TPrlyLeuArgPheIleGlyIle 240
Db      999 GAGTCCCATGACCGCAGCGCAAGAAAAGCCATCACCAAGAAAGATTAATTTGTGTATC 1058
Qy      241 ArgMetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAspHe 260
Db      1059 CGAATGATGTCTACTACGTCGACCAAGCAAGCTGAAGAGACCGGACCGGACTTC 1118
Qy      261 ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg 280

```


Db	1119	CCAGACGCGATCTCAGGAGCGGTATATATGTAAAGTAATTCCTGATACCCGACGAGAACT	1178
Qy	281	GLYGLYLLEGIINAPGLYASPILELLEVALYSLANGIYARGPROLEUVALASPSEK	300
Db	1179	GGTGATCTCAAGGAAAACGACGTCTATATCAGCATCATGACAGCTCGGTGCTCCGCC	1238
Qy	301	SERGLNLEUGINGLUNLAVALLLEUTHRCGLUSERPROLEULEUGLUNLAVLARGGLY	320
Db	1239	AATGATGTCACCGACGTCATTMAAAGGAAAAGCACCCCTGAAACATGTGTGTCGCGAGGGGT	1298
Qy	321	ASNAAPASPLEULEUPHESERILEALAPROGLUVALVAL	333
Db	1299	AATGAAAGTATCATGATCACAGTGATTTCCGACGAATAAT	1337

```

RESULT 4
US-11-091-883-91
? Sequence 91, Application US/11091883
? Publication No. US20060024693A1
? GENERAL INFORMATION:
? APPLICANT: CIBIEL, JOSE
? APPLICANT: FERNANDEZ, EMILIO O.
? APPLICANT: JORDAO DE MEGALHAES, GUILHERME
? APPLICANT: KOCABAS, ARI F.
? APPLICANT: CROSBY, JAVIER A.
? TITLE OF INVENTION: IDENTIFICATION OF GENES OR POLYPEPTIDES THE EXPRESSION OF WHICH
? TITLE OF INVENTION: CORRELATES TO FERTILITY, OVARIAN FUNCTION AND/OR FETAL/NEONORNAL
? TITLE OF INVENTION: VIABILITY
? FILE REFERENCE: 53942US
? CURRENT APPLICATION NUMBER: US/11/091,883
? CURRENT FILING DATE: 2005-03-29
? PRIOR APPLICATION NUMBER: 60/556,875
? PRIOR FILING DATE: 2004-03-29
? NUMBER OF SEQ ID NOS: 513
? SOFTWARE: PatentIn version 3.3
? SEQ ID NO 91
? LENGTH: 2036
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-11-091-883-91

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Alignment Scores:		
Pred. No.:	4,276-114	Length: 2036
Score:	1034.50	Matches: 206
Percent Similarity:	80.28	Conservative: 61
Best Local Similarity:	61.98	Mismatches: 57
Query Match:	61.64	Indels: 10
DB:	12	Gaps: 2

US-10-617-443B-2 (1-334) X US-11-091-883-91 (1-2036)

[illegible]

QY	124	leuileuglyH1sSerAlaAspLeuArgProGlyGluPheValValAla11leGlySerPro	143
Db	844	CTGCTGGCCCGCTCCTCAAGACTGGCGCGGAGAGATTGCGTGTGCCATCGGAAGCCGC	903
QY	144	PheAlaIeuGlnAserThrValThrThrglyIleValSerThrAlaGlnArgGluIyArg	163
Db	904	TTTTCCCTTCAAAACACAGTCACCACCGGGATCGTAGACACCACCCAAGCGGCAAA	963
QY	164	GluIeuGlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAla11leLeuSerTyr	183
Db	964	GAGCTGGGGGCTCCGCAACTCAGACATGACATCACTCAAGCCAGCGCATCTCAACTAT	1022
QY	184	GlyAsnSerGlyGlyProLeuValAsnLeuAspGlyGluVal11leGlyIleAsnThrIleu	203
Db	1024	CGAAACTCGGAGGCGCCGTATTGTAACCTGACCGGTGAAGATTTGAATTAACCTTGC	1083
QY	204	LysValThrAlaGlyIleSerPheAla11leProSerAspArgIleThrArgPheLeuThr	223
Db	1084	AAATGTACAGCTGGAGATCTCTTGGCAATCCCATCTGATTAAGATTAAAAAGTTCCCTCAG	1144
QY	224	GluPheGlnAspLysGlnIleLeuAsp-----TrrpLysArgPheIleGlyIle	240
Db	1144	GAGTCCCATGACCGACAGCGCCAAAGAAAGAACCATCAACAAAGAAAGATTAATTTGGTATC	1203
QY	241	ArgMetArgThrIleThrProSerLeuValAspGluLeuLysAlaSerAsnProAspPhe	260
Db	1204	CGAATGATGTCACTCAAGTCACGAGCAAGAAAGCAAAAGAGCTGAAGAGCAACCGGACCTTC	1265
QY	261	ProGluValSerSerGlyIleTyrValGlnGluValAlaProAsnSerProSerGlnArg	280
Db	1264	CCAACTCGTACTCAGAGCGCTAATATTAATGAAAGTAATCTCTGATTAACCCACGCAAACT	1322
QY	281	GlyGlyIleGlnAspGlyAspIleIleValLysValAsnGlyArgProLeuValAspSer	300
Db	1324	GGTGGTCTCAAGAAAGAGACGTCAATATACGATCAATGACAGCTCCGTGTCTCCGCC	1383
QY	301	SerGluLeuGlnGluValValLeuThrGluSerProLeuLeuGluValAlaArgArgIly	320
Db	1384	AATGATGTCAAGCGACTCATTAATAAGGAAAGCAACCTCGAACATGATGTGTCCGACGGGT	1443
QY	321	AsnAspAspLeuLeuPheSerIleAlaProGluValVal	333
Db	1444	AATGAAGATATCATGATCAACAGTATTTCCGGAAGAAATTT	1482

RESULT 5
 US-11-183-914-23
 Sequence 23, Application US/11183914
 Publication No. US20050282214A1
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 APPLICANT: Guergler, Karl J.
 APPLICANT: Corley, Neil C.
 APPLICANT: Tang, Tom Y.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Fastseq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/11/183,914

FILING DATE: 19-JULY-2005
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/008,271
 FILING DATE: 16-Jan-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Mohan-Peterson, Sheela
 REGISTRATION NUMBER: 41,201
 REFERENCE/DOCKET NUMBER: PF-0458 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2476 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: SINITUCT01
 CLONE: 2680548
 US-11-183-914-23

Alignment Scores:
 Pred. No.: 1,376-95 Length: 2476
 Score: 882.00 Matches: 169
 Percent Similarity: 74.84 Conservative: 72
 Best Local Similarity: 52.54 Mismatches: 71
 Query Match: 52.54 Indels: 10
 DB: 12 Gaps: 2

US-10-617-443B-2 (1-334) x US-11-183-914-23 (1-2476)

QY 15 SerSerProArgTyLysPheAsnPhelIleAlaPheValGluLysIleAlaProAla 34
 DB 481 GCTTCTCCCGAGTCAGTACACTTCATCGAGATGCTGAGAGAAGACGACCTCC 540
 QY 35 ValValHisIleGluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSer 54
 DB 541 GTGGCTATATCGAATCTCGACCGGACCTTTCTTGGGCGCGAGGTCCTATCTCG 600
 QY 55 SerGlySerGlyPheIleMetSerGluAlaGlyLeuIleIleThrAsnAlaHisValAla 74
 DB 601 AACGCTCAGGATTTGCTGGCTGCCATGGCTCATTTGTACCAACGCCCATGTGGTG 660
 QY 75 SerSerAsnSerAlaAlaProGlyLysArgGlnLeuLysValGlnLeuGlnAsnGlyAsp 94
 DB 661 GCTGAT-----CGGCGCAGAGTCCTGTGAGACTGCTAAGCGGCGAC 702
 QY 95 SerTyrgLysAlaThrIleLysAspIleAspLysLysSerAspIleAlaThrIleLysIle 114
 DB 703 ACGTATGAGCGCGGTGTCAACAGCTGTGATCCCGTGGCAGACATCGCAACGCTGAGATT 762
 QY 115 HisProLysLysLysLeuProValLeuLeuLeuGlnHisSerAlaAspLeuArgProGly 134
 DB 763 CAGACTAAGGACCTCTCCCAACGCTGCTGGGACGCTGATGTCCGAGAAAGG 822
 QY 135 GluPheValValAlaIleGlySerProPheAlaLeuGlnAsnThrValThrThrGlyIle 154
 DB 823 GAGTTTGTGTTGCCATGGGAAGTCCCTTTCGACTCGCAGAACATCATCATCCGGCAT 882
 QY 155 ValSerThrAlaGlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTy 174
 DB 883 GTTACTCTGCTCAACGCTCAACAGAGACTGGGACTCCCAACCAATGTGAATAC 942
 QY 175 IleglnThrAspAlaIleIleAsnTyrgLysAsnSerGlyGlyProLeuValAsnLeuSer 194
 DB 943 ATTCAACTGAGAGCTATTTGATTTTGAACCTGGAGGTCCTCGGTAACTGAT 1002
 QY 195 GlyGluValIleGlyIleAsnThrLeuLysValThrAlaGlyIleSerPheAlaIlePro 214

DB 1003 GGGGAGTGATTGGATGTGAACACCATGAGGTCAAGCTGGAATCTCTTGCATCCCT 1062
 QY 215 SerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln-----Ile 230
 DB 1063 TCTGATGCTCTTCAGAGACTTCTGATCTGTGGGAAAAGAAAGAAATCTCTCCGGAAATC 1122
 QY 231 LysAspTrpLysLysArgPheIleGlyIleArgMetArgThrIleThrProSerLeuVal 250
 DB 1123 AGTGGTCCCAAGCGCGCTACATTGGGGGTGATGATGTCGACCTCGAGTCCAGCATCTCT 1182
 QY 251 AspGluLeuLysAlaSerAsnProAspPheProGluValSerSerGlyIleTyValGln 270
 DB 1183 GCTGAACCTACAGCTTTCAGAACCAAGCTTCCCATGTTCCAGATGGGTGATCTACAT 1242
 QY 271 GluValAlaProAsnSerProSerGluArgGlyGlyIleGlnAspGlyAspIleIleVal 290
 DB 1243 AAGTCATCTCGGGCTCCCTCGACACCGGGCTGTGCTGGCGCTGGAGTGAATTTTG 1302
 QY 291 LysValAsnGlyArgProLeuValAspSerSerGluLeuGlnGluAlaValLeuThrGlu 310
 DB 1303 GCCATGGGAGCAGCATGTGTCAAAATGCTGAAGTGTATTGAAGCTTTCGAACCA 1362
 QY 311 SerProLeuLeuGluValArgArgGlyLysAspAspLeuLeuPheSerIleAlaPro 330
 DB 1363 TCCCATGTCGACGTGACATCCGGCGGACGAGAACACATGACCTTATATGTACCCCT 1422
 QY 331 GluVal 332
 DB 1423 GAGGTC 1428
 RESULT 6
 US-10-467-657-2095
 Sequence 2095, Application US/10467657
 Publication No. US20050260581A1
 GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 APPLICANT: FONTANA Maria Rita
 APPLICANT: PIZZA Mariagrazia
 APPLICANT: MASTIGNANI Vega
 APPLICANT: MONACI Elisabetta
 TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/467,657
 PRIOR FILING DATE: 2003-08-11
 PRIOR APPLICATION NUMBER: GB-0103424.8
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: Seqwin99, version 1.04
 SEQ ID NO 2095
 LENGTH: 1497
 TYPE: DNA
 ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-2095
 Alignment Scores:
 Pred. No.: 2,056-39 Length: 1497
 Score: 414.00 Matches: 112
 Percent Similarity: 51.24 Conservative: 58
 Best Local Similarity: 33.74 Mismatches: 98
 Query Match: 24.74 Indels: 64
 DB: 8 Gaps: 10
 US-10-617-443B-2 (1-334) x US-10-467-657-2095 (1-1497)
 QY 25 AlaAspValValGluLysIleAlaProAlaValHisIleGluLeu----- 40
 DB 172 GCCCAACTGTTCAAAAGGAAGCCCGGCACTGTCAATATTACGACGCCGCCGCCG 231
 QY 40 ----- 40
 DB 232 CGCAACCCAAAACGGCAGCGGCAATGCCGAAAACGATTCGACCCGCTTGGCAGACGAC 291
 QY 41 ---PheLeuArgHisProLeuPheGlyArgAsnValPro----- 52

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Db      292 CCGTTC-----TACGAATTTTCAACCGCTCGTCCGACACATGCCCGAATCCCCCA 345
Qy      53 -----leuserSerglySerglyPheIleMetSerglyAglly 65
Db      346 GAAGAAGACAGATGACCGCGGATTTGAACCTTCGGGGCTTCATCATGACAAAACCGGC 405
Qy      66 LeuIleIleThraSrnAlaHisValValSerSerAmsSeraAlaIarProGlyArgGlnGln 85
Db      406 TACATCTGACCAATACCCACGTCGTTCG-----GATATGGGCACT 447
Qy      86 LeuLyValGlnLeuGlnAmsnglyAaspSerglyGluAlaThrIleLySapIleApyLy 105
Db      448 ATCAAAAGTCCTGCTGCAACGACGACGCGAATATACGCCAAATCATCGGTCGATGTC 507
Qy      106 LySerAapIleAlaThrIleLySIIeHISpRoLybLyelyleuProValLeuLeuLeu 125
Db      508 CAATCCGATGTCGCTTCGAAAATCGACGCAACCGAAGAGCTACCCGTCGCAAAAATC 567
Qy      126 GlyHisSeraAlaAapLeuAarProGlyGluPheValAlaIleGlySerProPheAla 145
Db      568 GGGAAATCCCAAAATTTGAAACCGGGCGAATGGGTGCTGCGCATCGCGCGCCCTTCGGC 627
Qy      146 LeuGlnAmsThrValThrThrGlyIleValSerThrAlaGlnArgGluGlyArgGluLeu 165
Db      628 TTTCACACAGCGGTGACCGCGCGCATCGTGTCCGCC-----AAAGCAGAAAGCCTG 678
Qy      166 GlyLeuAarAapSerAapMetApyrIleGlnThrAapAlaIleIleAmsIlyrGlyAan 185
Db      679 CCC---AAGCAAGCTACACACCCCTTCATCCAAACGACGTCGTCATCATCGGGCAAT 735
Qy      186 SerGlyGlyProLeuValAmsLeuAapGlyGluValIleGlyIleAmsThrLeuLySVal 205
Db      736 TCGCGGCGCCCTGCTTCAACTTAAAGACAGGTGTGCGCATCAATTCGCAAAATATAC 795
Qy      206 Thr-----AlaGlyIleSerPheAlaIleProSerAapThrIleThrArg 220
Db      796 AGCGCAGCGCGCGATTCATGCGCATCTCCTTGCCATCCGCAATGAC---GTTCGCATG 852
Qy      221 PheLeuThrGluPheGlnApyrGlnIleLyAapTrpLyelyleuArgPheIleGlyIle 240
Db      853 AATGTGCGGAA---CAGCTGAAAACACCGCGCAAAATCCACGCGACACATCGGGCGTG 909
Qy      241 ArgMetAarThrIleThrProSerLeuValAapGluLeuLybAlaSerAmsProAapPhe 260
Db      910 ATTATTCAGAAAGTATCTTACGCTTTGGCAGACGCTCGTGGCTG----- 954
Qy      261 ProGluValSerSerglyIleTyValGlnGluValAlaProAmsSerProSerglyArg 280
Db      955 ---GATTAAGCCAGCGCGCGCATGATGCAAAATCCTTCGCGGACGCCCGCAGAACGT 1011
Qy      281 GlyGlyIleGlnAapGlyAapIleIleValLySValAmsnglyAarProLeuValAapSer 300
Db      1012 GCCGGCTTCACGCGCGGCGACATCGTCTCAGCTCGACGCGGAGAAAATACGTTCTTCC 1071
Qy      301 SerGluLeuGlnGluValLeuThrGluSerPro 312
Db      1072 GCGGACCTTCCTCATGCTCGCGCCCATTAACGCCG 1107

RESULT 7
US-11-098-686-9246
; Sequence 9246, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
```

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; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9246
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-11-098-686-9246

Alignment Scores:
Pred. No.: 5,846-39 Length: 1425
Score: 410.00 Matches: 94
Percent Similarity: 57.4% Conservative: 58
Best Local Similarity: 35.5% Mismatches: 89
Query Match: 24.4% Indels: 24
DB: 12 Gaps: 7

US-10-617-443B-2 (1-334) x US-11-098-686-9246 (1-1425)
Qy      54 SerSerglySerglyPheIleMetSerglyAgllyLeuIleIleThraSrnAlaHisVal 73
Db      271 TCATTAGAACTGCTTTATCTTCTTCAGATGATATATTGTTACCAATATATCATGTG 330
Qy      74 ValSerSerAmsSeraAlaIarProGlyArgGlnGlnLeuLySValGlnLeuGln----- 91
Db      331 ATAGAA-----GGACGAGATTCGTAGAGTAAATCTGAAGGTACC 372
Qy      92 -----AmsnglyAapSerglyGluAlaThrIleLySapIleApyLySerglyPhe 109
Db      373 TCAGCAAAAGAAATCTACCTGACAGAGATGATAGTAGAATGAAGAAACAGATCTT 432
Qy      110 AlaThrIleLySIIeHISpRoLybLyelyleuProValLeuLeuGlnGlyHisSeraAla 129
Db      433 GCTTATTAAAGTTAAAGTAAAGTACATTCATTCTTATATTGGAATATCAGAT 492
Qy      130 AapLeuAarProGlyGluPheValAlaIleGlySerProPheAlaLeuGlnAmsThr 149
Db      493 ACTATGAAAGTTGGATGATGGTGTGCTACCTATGGTAAATCCTTTGGCTTAGGCCATACA 552
Qy      150 ValThrThrGlyIleValSerThrAlaGlnArgGluGlyAarGlyLeuAarAap 169
Db      553 GTTACAGCAGTAAATTAATGATGCT-----AAAGCAGTAAATTCATGCTGGACCA 603
Qy      170 SerAapMetApyrIleGlnThrAapAlaIleIleAmsIlyrGlyAmsSerglyPhePro 189
Db      604 TTTGAT---AAGCTTTTCAAACTGATGATCTATCAATCTCGGGAATATAGTGTGTCCA 660
Qy      190 LeuValAmsLeuAapGlyGluValIleGlyIleAmsThrLeuLySValThrAla----- 207
Db      661 TTAATCAATATGTCAGCAAAAGTTGTAGCATTAACACAGCTAATTATGCAAGTGGCAG 720
Qy      208 GlyIleSerPheAlaIleProSerAapThrIleThrAapPheLeuThrGluPheGlnAap 227
Db      721 GGTATGTGTTTCGCTATCCCAAGTAAATGATGCGACATCTAATTATTAAGCCAGTTA----- 774
Qy      228 LySglnIleLyAapTrpLyelyleuArgPheIleGlyIleAarMetAarThrIleThrPro 247
Db      775 AAGCAAAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 834
Qy      248 SerLeuValAapGluLeuLybAlaSerAmsProAapPheProGluValSerSerglyIle 267
Db      835 AATACAGCTAAAGCTCTTGATATCTCAG-----GCAAAAGGTCCG 876
Qy      268 TyrValGlnGluValAlaProAmsSerProSerglyArgGlyIleGlnAapGlyAap 287
Db      877 CTGTGAGTCTGTTGTTCTCGAGACATCTGTAAGCGCTGCTTAAGGTTGGCAAT 936
Qy      288 IleIleValLySValAmsnglyAarProLeuValAapSerSerglyLeuGlnGluValAla 307
Db      937 ATTGTAAACAAGCTGATGTAACAATTAATGATGCAAGCTCATTTTAAAGCTAATT 996
Qy      308 LeuThrGluSerPro 312
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Db 997 GCTACTAAACCTCCT 1011

RESULT 8

US-11-098-686-8739/c

Sequence 8739, Application US/11098686

Publication No. US20060024696A1

GENERAL INFORMATION:

APPLICANT: Kapur, Vivek and Gebhart, Connie J.

TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES

FILE REFERENCE: 09531-128001

CURRENT FILING DATE: 2005-04-04

PRIOR FILING DATE: 2003-10-01

PRIOR APPLICATION NUMBER: PCT/US03/31318

PRIOR FILING DATE: 2003-10-01

NUMBER OF SEQ ID NOS: 11433

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8739

LENGTH: 1457619

TYPE: DNA

ORGANISM: Lawsonia intracellularis

US-11-098-686-8739

Alignment Scores:

Pred. No.: 4.42e-35 Length: 1457619

Score: 410.00 Matches: 94

Percent Similarity: 57.44 Conservative: 58

Best Local Similarity: 35.54 Mismatches: 89

Query Match: 24.44 Indels: 24

Gaps: 7

US-10-617-443B-2 (1-334) x US-11-098-686-8739 (1-1457619)

Qy 54 SerSerGlySerGlyPheIleIleSerGluAlaGlyLeuIleIleThrAsnAlaIleVal 73

Db 434347 TCATTATGAGACGCTTTATCATCTTCTCAGATGATATATGTTACCAATATCATGTG 434288

Qy 74 ValSerSerAsnSerAlaIleProGlyArgGlnGlnLeuValGlnLeuGln----- 91

Db 434287 ATAGAA-----CGACGACATCTCTGTAAGTAATCTGAAGTACC 434246

Qy 92 -----AenglyAspSerTyrcIuAlaIleIleValIleAspIleAspIleAspIle 109

Db 434245 TCAGCAAAAGAAATCACTACCTCAGAGATGATGATGATGATGATGATGATGATGAT 434186

Qy 110 AlaThrIleIleValIleProIleIleValIleProIleIleValIleProIleIleVal 129

Db 434185 GCTTATTAATAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 434126

Qy 130 AspLeuArgProGlyGluPheValAlaIleGlySerProPheAlaLeuGlnAsnThr 149

Db 434125 ACTATGGAAGTGGTGAATGGGTGCTAGCTATGTAATCTTTGGGTAGGCATACA 434066

Qy 150 ValThrThrGlyIleValSerThrAlaGlnArgGlnGlnGlnGlnGlnGlnGlnGln 169

Db 434065 GTTACAGCAGATATTAAGTCT-----AAAGACGATATTCATGCTGACCA 434015

Qy 170 SerAspMetAspTyrcIleIleIleIleIleIleIleIleIleIleIleIleIleIle 189

Db 434014 TTTGAT---AAGTTTAAACATGATGATGATGATGATGATGATGATGATGATGATGAT 433958

Qy 190 LeuValAsnLeuAspGlyGluValIleGlyIleAsnThrLeuValThrAla----- 207

Db 433957 TTAATCAATATGTCAGCAAGATGCTAGCATTAACACAGCTATTAATGCAAGTGGCA 433898

Qy 208 GlyIleSerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAsp 227

Db 433897 GGTATTTGGTTTGGCTATCCCAAGATGATGATGATGATGATGATGATGATGATGATGAT 433844

Qy 228 LysGlnIleIleValAspTrpLysLeuPheIleGlyIleArgMetArgThrIleThrPro 247

Db 433843 AAGACAATTAATAAGTAAGTAGAGTGTGATGATGATGATGATGATGATGATGAT 433784

Qy 248 SerLeuValAspGluLeuValAlaSerAsnProAspPheProGluValSerSerGlyIle 267

Db 433783 AATACAGCTAAAGCTCTGTGATTAATCTCAG-----GCATAAGTGGC 433742

Qy 268 TyrValGlnGluValAlaProAsnSerProSerGlnArgGlyIleGlnAspGlyAsp 287

Db 433741 CTGTAGGTTCTGTTCTCTCGAGATCTCTGATTAAGCGTCTTAAGTTGGCAT 433682

Qy 288 IleIleValIleValAsnGlyArgProLeuValAspSerSerGlyLeuGlnGlnAlaVal 307

Db 433681 ATTGTAAACAAGCTGATGATTAACAATGTATGATGATGATGATGATGATGATGATGAT 433622

Qy 308 LeuThrGluSerPro 312

Db 433621 GCTACTAAACCTCCT 433607

RESULT 9

US-10-454-437-55

Sequence 55, Application US/10454437

Publication No. US20050277115A1

GENERAL INFORMATION:

APPLICANT: Pompejus, Markus

APPLICANT: Krogger, Burkhard

APPLICANT: Zelder, Oskar

APPLICANT: Habermeyer, Gregor

TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS

FILE REFERENCE: BGI-128PCPN

CURRENT FILING DATE: US/10/454,437

PRIOR FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: US 60/141031

PRIOR FILING DATE: 1999-06-25

PRIOR APPLICATION NUMBER: DE 19931636.8

PRIOR FILING DATE: 1999-07-08

PRIOR APPLICATION NUMBER: DE 19932125.6

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932126.4

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932127.2

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932128.0

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932129.9

PRIOR FILING DATE: 1999-07-19

PRIOR APPLICATION NUMBER: DE 19932226.0

PRIOR FILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: DE 19932920.6

PRIOR FILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: DE 19932922.2

PRIOR FILING DATE: 1999-07-14

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 442

SEQ ID NO 55

LENGTH: 1446

TYPE: DNA

ORGANISM: Corynebacterium glutamicum

FEATURE:

NAME/KEY: CDS

LOCATION: (101)..(1423)

OTHER INFORMATION: RXA02630

US-10-454-437-55

Alignment Scores:

Pred. No.: 5.57e-33 Length: 1446

Score: 360.50 Matches: 101

Percent Similarity: 49.58 Conservative: 44

Best Local Similarity: 34.58 Mismatches: 97

Query Match: 21.58 Indels: 51

Gaps: 9

US-10-617-443B-2 (1-334) x US-10-454-437-55 (1-1446)

QY 27 ValValaGluValaIleAlaProAlaValaIleGluLeuPheLeuArgHisProLeu 46
 536 GTTGGCGCGAGCTTTGCTCTGCTCTCTATTCAGCGCATTAAGG----- 586

QY 47 PheGlyArgAsnValProLeuSerSerGlySerGlyPheIleMetSerGlyValaGlyLeu 66
 587 -----ACGCTGCTCTCTGAGGCTCTGATCATTAATTTCTCTGATGTTAC 634

QY 67 IleIleThrAsnAlaHisValaValaSerAsnSerAlaAlaProGlyArgGlnIn--- 85
 635 GTCATGACCAATATACATCGTCGAGCA-----GGCATTTGACAACTCT 676

QY 86 -----LeuLysValaGluLeuGlnAsnGlyAspSerTyrGluAlaThrIleLysAspIle 103
 677 GGTGTGTAGAAAGTATGTTCTCCGATGGAACCTACGCCAAGCTGATTTATTCCTGCT 736

QY 104 AspLysLysSerAspIleAlaThrIleLysIleHisProLysLysLeuProValLeu 123
 737 GATCCTTCCACATATTTGCTGTGATTCAGATTAGGATGTGTCMACTTCAGTTTATG 796

QY 124 LeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValaValaIleGlySerPro 143
 797 AGCTTGGAGATTCCGACGCAATTAGCGTTGACAAAGTGTGATGCTGTGTTCTCCA 856

QY 144 PheAlaLeuGlnAsnThrValaThrThrGlyIleValaSerThrAlaGlnArgGluArg 163
 857 CTGGGTCTGAGCTTCATCTGACACCGGATATTGTGTGGCGCGTGAACGCTCTGTGCA 916

QY 164 GluLeu-----GlyLeuArgAspSerAspMetAspTyrIleGlnThrAspAlaIle 181
 917 GCTTCTGTGATGCGGAGAGTCTCCCTCATCATGCTCTATCCAGACCGATGCTGAGTC 976

QY 182 AsnTyrGlyAsnSerGlyGlyProLeuValaAsnLeuAspGlyGluValaIleGlyIleAsn 201
 977 AACCTGCTAACTCTGTGGTGGTCCGCTGTGATGTGATGGCAACCTCATTTGGCATGAAT 1036

QY 202 ThrLeuLysVala-----ThrAlaGlyIleSerPhe 211
 1037 TCGGTATTTGCATCGATTTCCAGACACGCGATTTCCGAGGTTCCATTTGATCTTGGTTT 1096

QY 212 AlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGlnIleLys 231
 1097 TCTATCCCATCCAC-----TTTCCCAAGCGCGTGGCCGATTCATGATCATCAGC 1144

QY 232 AspTrpLys-----LysArgPheIleGlyIleArgMetArgThrIleProSerLeu 249
 1145 ACCGGCCAGTAACTCAGCCGATGATCGGTGGCAGGTGGCACT----- 1189

QY 250 ValaAspGluLeuLysAlaSerAsnProAspPheProGlyValaSerSerGlyIleTyrVal 269
 1190 -----GACAACTCAGTACAGCGCGCTGTATT 1216

QY 270 GlnGluValaIleAlaProAsnSerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIle 289
 1217 GCCAGTGTTCAGAGTGTGACCGCGCAGATGCTGAGCTTCAGCCAGCGGATTCGTG 1276

QY 290 ValLysValaAsnGlyArgProLeuValaAspSerSerGly 302
 1277 ACCAAGCTCATGATCGA---GTATGTATGATGCCAGAC 1312

DB 1277 ACCAAGCTCATGATCGA---GTATGTATGATGCCAGAC 1312

RESULT 10
 US-10-793-626-3848
 ; Sequence 3848, Application US/10793626
 ; Publication No. US20050255478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMBERLY, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: PUI480US
 ; CURRENT APPLICATION NUMBER: US/10/793,626
 ; CURRENT FILING DATE: 2004-03-04
 ; PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3848
 ; LENGTH: 3007
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURES:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; US-10-793-626-3848

Alignment Scores:
 Pred. NO.: 6,08e-31 Length: 3007
 Score: 347.00 Matches: 94
 Percent Similarity: 50.9% Conservative: 72
 Best Local Similarity: 28.8% Mismatches: 104
 Query Match: 20.7% Indels: 56
 DB: Gaps: 11

US-10-617-443B-2 (1-334) x US-10-793-626-3848 (1-3007)

QY 8 SerAlaGlyLeuHisGlnLeuSerSerProArgTyrIlePheAsnPheIleAlaAspVal 27
 56 AGTCATGTGCGCATCATGTTAGTGTAAAGTAATCAATCAATCAATGATGATG 115

QY 28 ValGluValaIleAlaProAlaValaValaIle----- 38
 116 ATTAAGACGCTTCTCCGCAATTGTGGCGGTATAAATGCAAAATCTACAACTT 175

QY 39 ---GluLeuPheLeuArgHisProLeuPheGlyArgAsnValProLeuSerSerGlySer 57
 176 GATGATTTATTCAACGATAGCATCTTAATCAAAAGAGCGGAATTTGTTCCGCTGTG 235

QY 58 GlyPheIleMetSerGly---AlaGlyLeuIleIleThrAsnAlaHisValaValaSerSer 76
 236 ATTATTCAAATTAAGTAAGTCTCCGATATATCGTTCAATTAATCAAGTTTGAT--- 292

QY 77 AsnSerAlaAlaProGlyArgGlnGlnLeuLysValaGlnLeuGlnAsnGlyAspSerTyr 96
 293 -----GGTCTTCGGAATTTAAAGTTCAACTACATTAATTCAAACCAAGTA 337

QY 97 GluAlaThrIleLysAspIleAspLysLysSerAspIleAlaThrIleLysIleHisPro 116
 338 GATGCCAATTAATAGCTAAAGACCCCTAACAGATTTGCTGTTCAAAATTAAGAT 397

QY 117 LysLysLysLeuProValaLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPhe 136
 398 ACAAAAGAAATAAAGCAATTCATTTGCTAATTCGTCAAAAGTTCAACAGAGATAGT 457

QY 137 ValValaIleIleGlySerProPheAlaLeuGln-----AsnThrValaThrThrGlyIle 154
 458 GTTTTTCAGACAGACCTGCAATTAATCCCGGTAATTCGGGTGCTGATTAAGCAAGAT 517

QY 155 ValSerThrAlaGlnArgGlu---GlyArgGluLeuGlyLeuArgAspSerAspMetAsp 173
 518 ATTTCAGCTAGCAACGTAATTCAGCCCAATTAATCTCTGCTGTAATCTAAAGTTAAT 577

QY 174 TyrIleGlnThrAspAlaIleIleAsnTyrGlyAsnSerGlyGlyProLeuValaAsnLeu 193
 578 GTTTTTCAGACAGACCTGCAATTAATCCCGGTAATTCGGGTGCTGATTAAGCAAGAT 637

QY 194 AspGlyGluValaIleGlyIleAsnThrLeuLysValaThrAla-----GlyIle 209
 638 AACGGAATCTCGTGTGATTCATTCATGAAATTCGCGCAGACCAAGTAGAAGGTATA 697

QY 210 SerPheAlaIleProSerAspArgIleThrArgPheLeuThrGluPheGlnAspLysGln 229
 698 GATTTCCTATACCTAGTAATGAAGTAGACCAATC-----GAACAATC 745

QY 230 IleLysAspTrpLys-----LysArgPheIleGlyIleArgMetArgThrIleThrPro 247
 746 GTTAACATGCTAATTAATGAAAGCCCTTCATGGGTATAGTCTTAATTAATTAAGT--- 802

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Qy 248 SerLeuValAepGluLeuLysAlaSerAenProAepPheProGlu----- 262
Db 803 -----GATATTCTGAAAGCAATCTGTAAGA 829
Qy 263 -----ValSerSerGlyIleTyrValGlnGluValAlaProAenSerProSer 278
Db 830 CTACATCTCATTAAGCAAGGCGTTTATGTAGCTAAAGTA-----GAC 874
Qy 279 GlnArgGlyGlyIleGlnAepGlyAapIleIleValAlaAenGlyAArgProLeuVal 298
Db 875 AGTGAATAATGCCATTAAAGGCGTATATTACTGAAATGATGATGAATCAATATAAA 934
Qy 299 AepSerSerGluLeuGln 304
Db 935 GATGATACGATTTAAGA 952

RESULT 11
US-10-793-626-3756/c
; Sequence 3756, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P03480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3756
; LENGTH: 3650
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-3756

Alignment Scores:
Pred. No.: 7,81e-31 Length: 3650
Score: 347.00 Matches: 94
Percent Similarity: 50.9% Conservative: 72
Best Local Similarity: 28.8% Mismatches: 104
Query Match: 20.7% Indels: 56
DB: 8 Gaps: 11

US-10-617-443B-2 (1-334) x US-10-793-626-3756 (1-3650)
Qy 8 SerAlaGlyLeuHsGlnLeuSerSerProArgTyrLysPheAenPheIleAlaApyAl 27
Db 1304 AGTCATGCTGCAATCACTGTGATGCTAAAGTAAATCAATCAATCAATGATGATGATG 1245
Qy 28 ValGluLysIleAlaProAlaValAlaHisIle----- 38
Db 1244 ATTAAGCGCTTCTCCCGCAATTTCCGCGGTGATGAATCAAGCAAAATCTACAAACCTT 1185
Qy 39 --GluLeuPheLeuAArgHisProLeuPheGlyArgAenValProLeuSerSerGlySer 57
Db 1184 GATGATTTATTCACGCGTAAGCATCTAAATCAAAAGAAAGCGGAATGTTCCGCTGTG 1125
Qy 58 GlyPheIleMetSerGlu--AlaGlyLeuIleIleThrAenAlaHisValValSerSer 76
Db 1124 ATTTATCAATTAAGAGGTTCCCGCATATTCGTTACAAATTAATCAAGTGTGTAT-- 1068
Qy 77 AenSerAlaAlaProGlyAArgGlnGlnLeuLysValGlnLeuGlnAenGlyAapSerTyr 96
Db 1067 -----GTTGCTTCGGAATTAAGTTCACTCACTCAATTAATCAAAACAGTA 1023
Qy 97 GluAlaThrIleLysAapIleAapLysLysSerAapIleAlaThrIleLysIleHisPro 116
Db 1022 GATGCCAAATTAATGTAAAGACGCCCTAACAGATATTGCTGTCTAAATAATAAGAT 963
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Qy 117 LysIleLysLeuProValLeuLeuLeuGlyHisSerAlaAapLysAArgProGlyGluPhe 136
Db 962 ACAAGAGAAATTAAGCAATTCATTAATTCCTAAATTCGCAAAAGTCAACAGAGAGTACT 903
Qy 137 ValValAlaIleGlySerProPheAlaLeuGln-----AenThrValThrThrGlyIle 154
Db 902 GTTTTTCGATGGGTAATCTCTAGATTAAGATTGCAAAATTCGTTAATCATCAAGAAAT 843
Qy 155 ValSerThrAlaGlnArgGlu--GlyAArgLeuLeuGlyLeuAArgSerAapMetAap 173
Db 842 ATTGAGCTACGCAAGTACATTAATGACCCCAATCTTCTGCTGTGTAATTAATTAATTAAT 783
Qy 174 TyrIleGlnThrAapAlaIleIleAapTyrGlyAenSerGlyGlyProLeuValAenLeu 193
Db 782 GTTTACAGACAGCGCTGCAATTAATCCGGTAATTCGGGTGTCATTAATGATTAAT 723
Qy 194 AepGlyGluValIleGlyIleAenThrLeuLysValThrAla-----GlyIle 209
Db 722 AACGGAATCTCGTGTGATCATTAATGCAAAATTTGGGCGACGACAGTAAGTAAGTATA 663
Qy 210 SerPheAlaIleProSerAapArgIleThrAArgPheLeuThrGluPheGlnAapLysGln 229
Db 662 GTTTTGTCTAATCCTAGTAATGAAGTTAGAGTGAACATC-----GAAACAATC 615
Qy 230 IleLysAapTyrLys-----LysAArgPheIleGlyIleArgMetAArgThrIleThrPro 247
Db 614 GTTAAACATGTGTAATGAAGCCCTCAATCGGTAAAGTCTTAATTAATTAAGT--- 558
Qy 248 SerLeuValAepGluLeuLysAlaSerAenProAepPheProGlu----- 262
Db 557 -----GATATTCTGAAAGCAATCTGTAAGA 531
Qy 263 -----ValSerSerGlyIleTyrValGlnGluValAlaProAenSerProSer 278
Db 530 CTACATCTCATTAAGCAAGGCGTTATGTAGCTAAAGTA-----GAC 486
Qy 279 GlnArgGlyGlyIleGlnAepGlyAapIleIleValLysValAenGlyAArgProLeuVal 298
Db 485 AGTGAATAATGCCATTAAAGGCGTATATTACTGGAATGATGATGAATCAATATAAA 426
Qy 299 AepSerSerGluLeuGln 304
Db 425 GATGATACGATTTAAGA 408

RESULT 12
US-11-074-176-3
; Sequence 3, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klienhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAniff, Olivia
; APPLICANT: Perill, Andrea Accarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Screens-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1269)
; NAME/KEY: misc_feature
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QY 226 GlnAspLySGlnIleLysAspTrpLys-----LysArgPheIleGlyIleArgMetArg 243
DB 592 ---GAACAACCTGTTAAACATGATGAATCGAACGCCCTTCAATGATGATAGTTTATA 648
QY 244 ThrIleThrProSerLeuValAspGluLeuLysAlaSerAspPheProGlu--- 262
DB 649 AATTAACT-----GATATTCTTAAAC 672
QY 263 -----ValSerGlyIleTyrrValGlnGluValAlaPro 274
DB 673 TATCGTAAAGACTACATCTCATTAAGACAAAGCGCTTATGATGATAAGTA----- 726
QY 275 AsnSerProSerGlnArgGlyGlyIleGlnAspGlyAspIleIleValLysValAsnGly 294
DB 727 -----GACAGTGAATAATGCCATTAAAGAGGTGATATTATTAATGAGATAGATGCT 777
QY 295 ArgProLeuValAspSerSerGluLeuGln 304
DB 778 AAACAAATTAATAAGATGATACAGATTAAAG 807

RESULT 14
US-10-750-185-32084
; Sequence 32084, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32084
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Bovine 19866881917166
US-10-750-185-32084

Alignment Scores:
Pred. No.: 9.02e-24 Length: 908
Score: 282.00 Matches: 56
Percent Similarity: 95.3% Conservative: 5
Best Local Similarity: 87.5% Mismatches: 3
Query Match: 16.8% Indels: 0
DB: 8 Gaps: 0

US-10-617-443b-2 (1-334) x US-10-750-185-32084 (1-908)
QY 119 LysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValAla 138
DB 438 AAGCTGCTGTGCTACTGCTTGGCGCTCTCGAGCTGCGGCGGAGAGTTCTGTGTC 497
QY 139 AlaIleGlySerProPheAlaLeuGlnAsnThrValThrThGlyIleValSerThrAla 158
DB 498 GCCATTGGAAGCCCTTTTCCCTTCAAAAACAGGTCAACACGGGATGCTGACACACC 557
QY 159 GlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrrIleGlnThrAsp 178
DB 558 CAGCTGTGTGCAAAAGAACTGGGGCTCCGGAATCGGACATGACTACATCCAGACAGAC 617
QY 179 AlaIleIleAsn 182
DB 618 GCCATCATCAAC 629
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RESULT 15
US-10-750-623-32084
; Sequence 32084, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32084
; LENGTH: 908
; TYPE: DNA
; ORGANISM: Bovine 19866881917166
US-10-750-623-32084

Alignment Scores:
Pred. No.: 9.02e-24 Length: 908
Score: 282.00 Matches: 56
Percent Similarity: 95.3% Conservative: 5
Best Local Similarity: 87.5% Mismatches: 3
Query Match: 16.8% Indels: 0
DB: 8 Gaps: 0

US-10-617-443b-2 (1-334) x US-10-750-623-32084 (1-908)
QY 119 LysLeuProValLeuLeuLeuGlyHisSerAlaAspLeuArgProGlyGluPheValAla 138
DB 438 AAGCTGCTGTGCTACTGCTTGGCGCTCTCGAGCTGCGGCGGAGAGTTCTGTGTC 497
QY 139 AlaIleGlySerProPheAlaLeuGlnAsnThrValThrThGlyIleValSerThrAla 158
DB 498 GCCATTGGAAGCCCTTTTCCCTTCAAAAACAGGTCAACACGGGATGCTGACACACC 557
QY 159 GlnArgGluGlyArgGluLeuGlyLeuArgAspSerAspMetAspTyrrIleGlnThrAsp 178
DB 558 CAGCTGTGTGCAAAAGAACTGGGGCTCCGGAATCGGACATGACTACATCCAGACAGAC 617
QY 179 AlaIleIleAsn 182
DB 618 GCCATCATCAAC 629

Search completed: February 21, 2006, 23:01:29
Job time : 937 secs
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